

Scoring table:	BLOSUM62	Gapext 10.0 , Gapext 0.5	Scorings:	US-10-612-818-4 1 RDGNPYAVCDKCLKFYSKISEY 22	Scorings:	US-10-612-818-4 1 RDGNPYAVCDKCLKFYSKISEY 22
Scorched:	1825181 seqs, 57537446 residues	Total number of hits satisfying chosen parameters:	1825181	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result score distribution. and is derived by analysis of the total score distribution.		
DB:	UniProt 02,* 1: uniprot_sprot: 2: uniprot_trembl: *	Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	SUMMARIES		
Database :				Description		
Result No.	Score	Query	Match	Length	DB ID	
1	125	100.0	81	2	Q80886	
2	125	100.0	84	2	Q80882	
3	125	100.0	90	2	Q80884	
4	125	100.0	90	2	Q80885	
5	125	100.0	91	2	Q80887	
6	125	100.0	99	2	Q919B2	
7	125	100.0	103	2	Q919D5	
8	125	100.0	130	2	Q919B4	
9	125	100.0	130	2	Q919B5	
10	125	100.0	130	2	Q919C0	
11	125	100.0	130	2	Q919C2	
12	125	100.0	130	2	Q919C8	
13	125	100.0	130	2	Q919D0	
14	125	100.0	138	2	Q919D2	
15	125	100.0	143	2	Q919B6	
16	125	100.0	143	2	Q919C4	
17	125	100.0	151	2	Q12335	
18	125	100.0	151	2	Q12336	
19	125	100.0	151	2	Q76780	
20	125	100.0	151	2	Q77816	
21	125	100.0	151	2	Q77JC7	
22	125	100.0	151	2	Q77JZ5	
23	125	100.0	151	2	Q77JZ5	
24	125	100.0	151	2	Q80966	
25	125	100.0	151	2	Q89640	
26	125	100.0	151	2	Q89648	
27	125	100.0	151	2	Q89708	
28	125	100.0	151	2	Q89755	
29	125	100.0	151	2	Q89852	
30	125	100.0	151	2	Q89887	
31	125	100.0	151	2	Q8B564	
32	125	100.0	151	2	Q8BB19	
33	125	100.0	151	2	Q8BB20	
34	125	100.0	151	2	Q8BB21	
35	125	100.0	151	2	Q9wC3	
36	125	100.0	151	2	Q9wC31	
37	125	100.0	151	2	Q9wMP2	
38	125	100.0	151	2	Q9wNP4	
39	125	100.0	151	2	Q9wNP5	
40	125	100.0	158	1	VE6 HPV16	
41	125	100.0	158	2	Q71b17	
42	125	100.0	158	2	Q8JUT8	
43	125	100.0	158	2	Q9wH13	
44	125	100.0	158	2	Q9QDH3	
45	125	100.0	158	2	Q9QDH9	

DR GO; GO:0001677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; .
 FT NON-TER 1 1
 SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896668E1CA CRC64;
 Query Match 100 0%; Score 125; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 6.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RDGNPFAVCDKCLKFYSKISY 22
 Db 11 RDGNPFAVCDKCLKFYSKISY 35

RESULT 3
 Q80884 PRELIMINARY; PRT; 90 AA.
 ID Q80884
 AC DT 01-NOV-1996 (TRMBMLrel. 01, Created)
 DT 01-NOV-1996 (TRMBMLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRMBMLrel. 25, Last annotation update)
 DT 01-NOV-1996 (TRMBMLrel. 01, Last annotation update)
 DE E6 protein (Fragment).
 DE Human Papillomavirus.
 OS Human papillomavirus, no RNA stage; Papillomaviridae;
 OC Viruses; ssDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=HPV16; TISSUE=Cervical tissue;
 RC Haegert D.G., Galutira D.P., Youngusband B.H.;
 RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U14516; AAB60570; 1.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR Go; GO:003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON-TER 1 1
 SQ SEQUENCE 91 AA; 11136 MW; 22DFDEA185ACBA7 CRC64;

Query Match 100 0%; Score 125; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPFAVCDKCLKFYSKISY 22
 Db 14 RDGNPFAVCDKCLKFYSKISY 35

RESULT 5
 Q80887 PRELIMINARY; PRT; 91 AA.
 ID Q80887
 AC DT 01-NOV-1996 (TRMBMLrel. 01, Created)
 DT 01-NOV-1996 (TRMBMLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRMBMLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human Papillomavirus.
 OC ssDNA viruses, no RNA stage; Papillomaviridae;
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=HPV16; TISSUE=Cervical tissue;
 RC Haegert D.G., Galutira D.P., Youngusband B.H.;
 RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U14516; AAB60570; 1.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR Go; GO:003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON-TER 1 1
 SQ SEQUENCE 91 AA; 11136 MW; 22DFDEA185ACBA7 CRC64;

Query Match 100 0%; Score 125; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPFAVCDKCLKFYSKISY 22
 Db 14 RDGNPFAVCDKCLKFYSKISY 35

RESULT 6
 Q919B2 PRELIMINARY; PRT; 99 AA.
 ID Q919B2
 AC DT 01-DEC-2001 (TRMBMLrel. 19, Created)
 DT 01-DEC-2001 (TRMBMLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TRMBMLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human Papillomavirus type 16.
 OC Viruses; ssDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=21846229; PubMed=11857370;
 RX Watts K.J., Thompson C.H., Cossett Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL EMBL; AP04704; AAL01365; 1.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR Go; GO:003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON-TER 1 1

RESULT 4
 Q80885 PRELIMINARY; PRT; 90 AA.
 ID Q80885
 AC DT 01-NOV-1996 (TRMBMLrel. 01, Created)
 DT 01-NOV-1996 (TRMBMLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRMBMLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus.
 OC Viruses; ssDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=HPV16; TISSUE=Cervical tissue;
 RC Haegert D.G., Galutira D.P., Youngusband B.H.;
 RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U14514; AAB60568; 1.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.

FT	NON_TER	99	99			SQ	SEQUENCE	130 AA;	15792 MW;	B6C2147D227EDDC CRC64;		
SQ	SEQUENCE	99 AA;	12005 MW;	C2B96025EE370B38	CRC64;							
Query Match		100.0%;	Score 125;	DB 2;	Length 99;		Query Match	100.0%;	Score 125;	DB 2;		
Best Local Similarity		100.0%;	Pred. No. 7.e-11;				Best Local Similarity	100.0%;	Pred. No. 1e-10;	Length 130;		
Matches		0;	Mismatches 0;	Indels 0;	Gaps 0;		Matches	22;	Conservative 0;	Mismatches 0;		
Qy		1 RDGNPYAVCDKCLKFYSKISEY 22				Oy		1 RDGNPYAVCDKCLKFYSKISEY 22		Indels 0;		
Db		31 RDGNPYAVCDKCLKFYSKISEY 52				Db		34 RDGNPYAVCDKCLKFYSKISEY 55		Gaps 0;		
RESULT 7												
Q919D6		PRELIMINARY;		PRT;	103 AA.		Q919B8		PRELIMINARY;	PRT;		
ID	Q919D6						ID	Q919B8		130 AA.		
AC	Q919D6:						AC	Q919B8;				
DT	01-DEC-2001	(TREMBLrel. 19,	Created)				DT	01-DEC-2001	(TREMBLrel. 19,	Created)		
DT	01-DEC-2001	(TREMBLrel. 19,	Last sequence update)				DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)		
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)				DS	B6 protein (Fragment).				
DE	Human papillomavirus type 16.						OS	Human papillomavirus type 16.				
OS	Human papillomavirus type 16.						Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;					
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;						CC	Papillomavirus.				
OC	Papillomavirus						NCBI_TaxID	10581;				
CX							RN	SEQUENCE FROM N.A.				
RN							RP	SEQUENCE FROM N.A.; PubMed=11857370;				
RP	SEQUENCE FROM N.A.; PubMed=11857370;						RX	MEDLINE=21846229;				
RX	MEDLINE=21846229;						RA	Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;				
RA	Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;						RT	"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";				
RT	"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";						RT	Int. J. Cancer 97:868-874 (2002).				
RT	cervical cancer 97:868-874 (2002).						DR	EMBL; AR04701; AAU013591; 1.				
RL	Int. J. Cancer 97:868-874 (2002).						DR	GO; GO:0042025; C:Host cell nucleus; IEA.				
DR	EMBL; AR04692; AAU01342.1; 1.						DR	GO; GO:003677; F:DNA binding; IEA.				
DR	GO; GO:0042025; C:Host cell nucleus; IEA.						DR	InterPro; IPR001334; E6.				
DR	DR InterPro; IPR001334; E6.						DR	Pfam; PF00518; E6; 1.				
DR	Pfam; PF00518; E6; 1.						FT	FT NON_TER	1	1		
FT	NON_TER	1	12422 MW;	6F90CBAB1F25449B	CRC64;	SQ	SEQUENCE	130 AA;	15775 MW;	92D3C07BF96B092F	CRC64;	
SQ	SEQUENCE	103 AA;					Query Match	100.0%;	Score 125;	DB 2;	Length 130;	
Query Match		100.0%;	Score 125;	DB 2;	Length 103;		Best Local Similarity	100.0%;	Pred. No. 1e-10;			
Best Local Similarity		100.0%;	Pred. No. 8e-11;				Matches	22;	Conservative 0;	Mismatches 0;	Indels 0;	
Matches		0;	Mismatches 0;	Indels 0;	Gaps 0;		Oy		1 RDGNPYAVCDKCLKFYSKISEY 22		Gaps 0;	
Qy		1 RDGNPYAVCDKCLKFYSKISEY 22					Db		34 RDGNPYAVCDKCLKFYSKISEY 55			
Db		7 RDGNPYAVCDKCLKFYSKISEY 28					RESULT 10					
RESULT 8												
Q919B4		PRELIMINARY;		PRT;	130 AA.		Q919C0		PRELIMINARY;	PRT;		
ID	Q919B4:						ID	Q919C0		130 AA.		
AC	Q919B4:						AC	Q919C0;				
DT	01-DEC-2001	(TREMBLrel. 19,	Created)				DT	01-DEC-2001	(TREMBLrel. 19,	Created)		
DT	01-OCT-2003	(TREMBLrel. 19,	Last sequence update)				DT	01-OCT-2003	(TREMBLrel. 25,	Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)				DS	B6 protein (Fragment).				
DE	Human papillomavirus type 16.						OS	Human papillomavirus type 16.				
OS	Human papillomavirus type 16.						Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;					
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;						OC	Papillomavirus.				
OC	Papillomavirus						NCBI_TaxID	10581;				
CX							RN	SEQUENCE FROM N.A.				
RN	SEQUENCE FROM N.A.; PubMed=11857370;						RP	MEDLINE=21846229;				
RX	MEDLINE=21846229;						RA	Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;				
RA	Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;						RT	"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";				
RT	"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";						RT	Int. J. Cancer 97:868-874 (2002).				
RT	cervical cancer 97:868-874 (2002).						DR	EMBL; AR04701; AAU013591; 1.				
DR	EMBL; AR04703; AAU01363.1; 1.						DR	GO; GO:0042025; C:Host cell nucleus; IEA.				
DR	GO; GO:0042025; C:Host cell nucleus; IEA.						DR	GO; GO:003677; F:DNA binding; IEA.				
DR	GO; GO:003677; F:DNA binding; IEA.						DR	InterPro; IPR001334; E6.				
DR	IPR001334; E6.						DR	Pfam; PF00518; E6; 1.				
FT	NON_TER	1	1			SQ	SEQUENCE	130 AA;	15779 MW;	26D0147D396B0929	CRC64;	

Query Match 100.0%; Score 125; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNNPVAVCDCKLKFKYSKISBY 22
Db 34 RDGNNPVAVCDCKLKFKYSKISBY 55

RESULT 11
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2; PRELIMINARY; PRT; 130 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 Protein (Fragment)
OS Human Papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus
OX NCBI_TAXID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874 (2002).
DR EMBL: AF44699; AAL01355.1;
GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR01334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNNPVAVCDCKLKFKYSKISBY 22
Db 34 RDGNNPVAVCDCKLKFKYSKISBY 55

RESULT 12
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8; PRELIMINARY; PRT; 130 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 Protein (Fragment)
OS Human Papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus
OX NCBI_TAXID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874 (2002).
DR EMBL: AF44696; AAL01349.1;
GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR01334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RDGNPYAVCDKCLKFYSKISYEY 22
 Db 42 RDGNPYAVCDKCLKFYSKISYEY 63

RESULT 15

Q919B6 PRELIMINARY; PRT; 143 AA.
 ID Q919B6; AC 0319B6;
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE B6 protein (Fragment).
 OS Human Papillomavirus type 16.
 OC Papillomaviridae; Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10581.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:21846329; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.,
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874 (2002).
 DR EMBL; AF04702; AAC01361.1;
 GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 InterPro:IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
 Query Match 100.0%; Score 125; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RDGNPYAVCDKCLKFYSKISYEY 22
 Db 47 RDGNPYAVCDKCLKFYSKISYEY 68

Search completed: November 22, 2004, 20:31:48
 Job time : 128.5 secs

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A;Molecule type: DNA
A;Residues: 1-149 <DNA>
A;Cross-references: UNIPROT:P27228; GB:M74117; NID:9333050; PID:AAA46966.1; PMID:9333051
R;Deinii, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36499
A;Accession: S36521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <DNA>
A;Cross-references: EMBL:X74477; NID:9396997; PID:9396998
A;Experimental source: strain 35H
C;Superfamily: Papillomavirus B6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 81.6%; Score 102; DB 1; Length 149;
Best Local Similarity 81.8%; Pred. No. 3e-07; Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RDGNNP^YAVCD^CLKFYSKISEY 22
Db 55 RDGNNP^YAVC^RCLLFYSKIREY 76

RESULT 3
W6WL51
E6 Protein - human papillomavirus type 51
C;Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40415
R;Langs, C.P.; Silverstein, S.J.
J.Virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 51
A;Reference number: A40415; MUID:9130375; PMID:1649326
A;Accession: E40415
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-151 <DNA>
A;Cross-references: UNIPROT:P26554; GB:M62877
C;Superfamily: Papillomavirus B6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 76.8%; Score 96; DB 1; Length 151;
Best Local Similarity 77.3%; Pred. No. 2.2e-06; Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RDGNNP^YAVCD^CLKFYSKISEY 22
Db 55 RDGNNP^YAVC^RCLLFYSKIREY 76

RESULT 4
W6WL58
E6 Protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence
A;Reference number: A36799; MUID:9024102; PMID:1656594
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <DNA>
A;Cross-references: UNIPROT:P26555; GB:D90400; NID:9222386; PIDN:BAA31845.1; PMID:93333709

C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 72.0%; Score 90; DB 1; Length 149;
Best Local Similarity 72.7%; Pred. No. 1.5e-05; Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RDGNNP^YAVCD^CLKFYSKISEY 22
Db 55 RDGNNP^YAVC^RCLLFYSKIREY 76

RESULT 5
A61237
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C;Accession: A61237
R;Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sijahurachman, A.; Warsa, U.
Int. J. Cancer 48, 516-522, 1991
A;Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma
A;Reference number: A61237; MUID:31258022; PMID:1646174
A;Accession: A61237
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <DNA>
C;Superfamily: papillomavirus E6 protein

Query Match 71.2%; Score 89; DB 2; Length 148;
Best Local Similarity 72.7%; Pred. No. 2.1e-05; Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 RDGNNP^YAVCD^CLKFYSKISEY 22
Db 55 RDGNNP^YAVC^RCLLFYSKIREY 76

RESULT 6
S36573
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36573
R;Delius, H.; Holmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36573
A;Molecule type: DNA
A;Residues: 1-149 <DNA>
A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:9397038; PIDN:CAA52585.1; PMID:9397038
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 71.2%; Score 89; DB 2; Length 148;
Best Local Similarity 72.7%; Pred. No. 2.1e-05; Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 RDGNNP^YAVCD^CLKFYSKISEY 22
Db 55 RDGNNP^YAVC^RCLLFYSKIREY 76

RESULT 7
W6WL31
E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A32444
R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989
 A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus. M.J.UJD:89299478; PMID:2545036.
 A;Accession: A32444
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-149 <COL>
 A;Cross-references: UNIPROT:P17386; GB:J04353; NID:9333048; PIDN:AAA46950_1; PID:g459916
 C;Comment: This protein may be involved in the oncogenic potential of this virus.
 C;Superfamily: Papillomavirus E6 protein
 P:30-66/Region: zinc finger CCCC motif
 P:103-139/Region: zinc finger CCCC motif

Query Match 70.4% Score 88; DB 1; Length 149;
 Best Local Similarity 63.6%; Pred. No. 2.9e-05;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 22
 Db 55 RDDTPHGVCTKLRFYSKVSF 76

RESULT 8

W6W133
 E6 Protein - human papillomavirus type 33
 C;Species: human papillomavirus type 33
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A03683
 R;Cole, S.T.; Streck, R.E.
 J;Virol. 58, 991-995, 1986
 A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh
 A;Reference number: A93020; MUID:86200464; PMID:300902
 A;Accession: A03683
 A;Molecule type: DNA
 A;Residues: 1-149 <COL>
 A;Cross-references: UNIPROT:P06427; GB:MI2732; NID:9333049; PIDN:AAA46958_1; PID:g463177
 C;Superfamily: Papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; zinc finger
 P:103-139/Region: zinc finger CCCC motif

Query Match 69.6% Score 87; DB 1; Length 149;
 Best Local Similarity 63.6%; Pred. No. 4e-05;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 22
 Db 55 REGPPFGICKLCLRFLSKISEY 76

RESULT 9

S36544
 E6 Protein - human papillomavirus type 26
 C;Species: human papillomavirus type 26
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S36544
 R;Delius, H.; Hofmann, B.,
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36544
 A;Residues: 1-150
 A;Cross-references: UNIPROT:P36807; EMBL:X74472; NID:g396956; PIDN:CAA52530_1; PID:g39695
 C;Keywords: early protein; zinc finger

Query Match 67.2% Score 84; DB 2; Length 150;
 Best Local Similarity 63.6%; Pred. No. 0.00011;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 22

RESULT 10

W6W139
 E6 Protein - human papillomavirus type 39
 C;Species: human papillomavirus type 39
 C;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: A38503
 R;Voiprav, C.; Streck, R.E.
 J;Virology 181, 419-423, 1991.
 A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
 A;Reference number: A38502; MUID:91135017; PMID:1847266
 A;Accession: A38502
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-158 <VOL>
 A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050_1;
 C;Superfamily: Papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 P:32-68/Region: zinc finger CCCC motif
 P:105-141/Region: zinc finger CCCC motif

Query Match 63.2% Score 79; DB 1; Length 158;
 Best Local Similarity 61.9%; Pred. No. 0.00057;
 Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 21
 Db 57 RDGEPLAACQSCIXFYAKIRE 77

RESULT 11

W6W143
 E6 Protein - human papillomavirus type 43
 C;Species: human papillomavirus type 43
 C;Note: host Homo sapiens (man)
 C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
 C;Accession: A34144
 R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
 J;Virol. 63, 2829-2834, 1989
 A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types associ

A;Reference number: A34144; MUID:93259065; PMID:2542593
A;Accession: A34144
A;Molecule type: DNA
A;Residues: 1-155 <LOB>
A;Cross-references: UNIPROT:PI19709 GB:M27022; NID:9341596; PIDN:AAA63453.1; PID:970347
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif

Query Match 61.5%; Score 77; DB 1; Length 155;
Best Local Similarity 59.1%; Pred. No. 0.0011; Mismatches 5; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

RESULT 15

Qy 1 RDGNPYAVCDKLFYKISKSY 22
Db 56 RDGYPPFAACLAQFHGKISKY 77

W6WL56

B6 protein - human Papillomavirus type 56
C;Species: human Papillomavirus type 56
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A33377; S36519
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Tempie, G.F.
J.Gen.Virol. 70, 3099-3104, 1989
A;Title: Human Papillomavirus type 56: a new virus detected in cervical cancers.
A;Reference number: A33377; MUID:90063558; PMID:2555440
A;Accession: A33377
A;Molecule type: DNA
A;Cross-references: UNIPROT:P24836
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: A33377
A;Accession: S36579
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <DBI>
A;Cross-references: EMBL:X74483; NID:9397053; PIDN:CAAS2596.1; PID:9397054
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;33-59/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif

Query Match 61.6%; Score 77; DB 1; Length 155;
Best Local Similarity 63.8%; Pred. No. 0.0011; Mismatches 6; Indels 0; Gaps 0;
Matches 14; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

RESULT 14

W6WLPR

B6 protein - human Papillomavirus type ME180 (provirus)
C;Species: human Papillomavirus type ME180
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: C40509
R;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Haesus, H.; Schwarz, E.
J.Virol. 65, 554-568, 1991
A;Title: Characterization of a novel human Papillomavirus DNA in the cervical carcinoma
A;Reference number: A40509; MUID:91374616; PMID:1716694.
A;Accession: C40509
A;Status: transposition not shown
A;Molecule type: DNA
A;Residues: 1-158 <REB1>
A;Cross-references: UNIPROT:P27962; GB:M732558
C;Superfamily: papillomavirus E6 protein

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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:32:01 ; Search time 97.5 Seconds
(without alignments)

Scoring table: BLOSUM62
GapOpen 10.0 , Gapext 0.5

Title: US-10-612-818-4

Perfect score: 125

Sequence: 1 RDGNPVAVCDKCLKFYKSKISEY 22

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
 1: /cgns2_6/ptodata/1/pubpa/US07_PUBCOMB.pep.*
 2: /cgns2_6/ptodata/1/pubpa/PCT_NEW_PUB.pep.*
 3: /cgns2_6/ptodata/1/pubpa/US06_PUB.pep.*
 4: /cgns2_6/ptodata/1/pubpa/US06_PUBCOMB.pep.*
 5: /cgns2_6/ptodata/1/pubpa/US07_PUB.pep.*
 6: /cgns2_6/ptodata/1/pubpa/PCTUS_PUBCOMB.pep.*
 7: /cgns2_6/ptodata/1/pubpa/US08_PUB.pep.*
 8: /cgns2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
 9: /cgns2_6/ptodata/1/pubpa/US09A_PUBCOMB.pep.*
 10: /cgns2_6/ptodata/1/pubpa/US09C_PUBCOMB.pep.*
 11: /cgns2_6/ptodata/1/pubpa/US10_PUBCOMB.pep.*
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 13: /cgns2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep.*
 14: /cgns2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
 15: /cgns2_6/ptodata/1/pubpa/US10D_PUBCOMB.pep.*
 16: /cgns2_6/ptodata/1/pubpa/US10E_PUBCOMB.pep.*
 17: /cgns2_6/ptodata/1/pubpa/US11_PUB.pep.*
 18: /cgns2_6/ptodata/1/pubpa/US11_NEW_PUB.pep.*
 19: /cgns2_6/ptodata/1/pubpa/US60_NEW_PUB.pep.*
 20: /cgns2_6/ptodata/1/pubpa/US60__PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	22	16	US-10-612-818-4
2	125	100.0	151	14	US-10-177-390-6
3	125	100.0	171	16	US-10-472-724-2
4	125	100.0	266	9	US-09-367-309A-1
5	125	100.0	273	13	US-10-000-903-4
6	125	100.0	292	13	US-10-000-903-10
7	125	100.0	371	13	US-10-000-903-6
8	125	100.0	390	13	US-10-000-903-14
9	109	87.2	170	16	US-10-476-570-11
10	71	56.8	172	16	US-10-472-724-6
11	71	56.8	278	13	US-10-000-903-21
12	71	56.8	383	13	US-10-000-903-23
13	61	48.8	10	8	US-08-344-824-237

ALIGNMENTS

RESULT 1
US-10-612-818-4
/ Sequence 4, Application US/10612818
/ Publication No. US20040110925A1
/ GENERAL INFORMATION:
/ APPLICANT: Impact Diagnostics
/ TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses for Detecting and/or Diagnosing Cervical and Other Human Papillomas
/ TITLE OF INVENTION: Associated Cancers
/ FILE REFERENCE: 3352-2-2
/ CURRENT APPLICATION NUMBER: US/10/612,818
/ CURRENT FILING DATE: 2003-07-01
/ PRIORITY NUMBER: US 60/394,172
/ PRIORITY FILING DATE: 2002-07-02
/ PRIORITY APPLICATION NUMBER: US 09-163687
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 4
/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE: OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
/ US-10-612-818-4

Query Match Score 125; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 1; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

OY 1 RDGNPVAVCDKCLKFYKSKISEY 22
Db 1 RDGNPVAVCDKCLKFYKSKISEY 22

RESULT 2

US-10-177-390-6

/ Sequence 6, Application US/10177390

/ PUBLIC INFORMATION:

/ APPLICANT: Schuierl, Gerold

/ TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear

/ TITLE OF INVENTION: Polymericlectides by Electroporation

/ FILE REFERENCE: 02150wo/JH/ml

/ CURRENT APPLICATION NUMBER: US/10/177,390

/ CURRENT FILING DATE: 2002-06-20

/ NUMBER OF SEQ ID NOS: 34

/ SOFTWARE: Patentin Ver. 2.1

/ SEQ ID NO 6

/ LENGTH: 151

/ TYPE: PRT

/ ORGANISM: Human papillomavirus type 16

us-10-177-390-6

Query Match 100.0%; Score 125; DB 16; Length 171;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 67 RDGNP₂A₁VCDKCLKFYSKIS₁Y 88

RESULT 3

US-10-472-724-2

/ Sequence 2, Application US/10472724

/ PUBLICATION NO. US20040171806A1

/ GENERAL INFORMATION:

/ APPLICANT: Cid-Arregui, Angel

/ APPLICANT: Zur Hause, Harald

/ TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination

/ FILE REFERENCE: 4121-154

/ CURRENT APPLICATION NUMBER: US/10/472,724

/ CURRENT FILING DATE: 2003-09-17

/ PRIOR APPLICATION NUMBER: PCT/EP02/03271

/ PRIOR FILING DATE: 2002-03-22

/ PRIOR APPLICATION NUMBER: EP 01107211.7

/ PRIOR FILING DATE: 2001-03-23

/ NUMBER OF SEQ ID NOS: 27

/ SOFTWARE: Patentin version 3.2

/ SEQ ID NO 2

/ LENGTH: 171

/ TYPE: PRT

/ FEATURE: Artificial sequence

/ OTHER INFORMATION: Synthetic Construct

us-10-472-724-2

Query Match 100.0%; Score 125; DB 16; Length 171;

Best Local Similarity 100.0%; Pred. No. 1.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 67 RDGNP₂A₁VCDKCLKFYSKIS₁Y 88

RESULT 4

US-09-367-309A-1

/ Sequence 1, Application US/09367309A

/ PUBLIC INFORMATION:

/ APPLICANT: MACFARLAN, RODERICK I.

/ APPLICANT: MALLIAROS, JIM

/ TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

/ FILE REFERENCE: 017227/0149

/ CURRENT APPLICATION NUMBER: US/09/367,309A

/ CURRENT FILING DATE: 1999-08-11

/ PRIOR APPLICATION NUMBER: PCT/AU98/00080

/ PRIOR FILING DATE: 1998-02-13

/ PRIOR APPLICATION NUMBER: AU PO 5178

/ PRIOR FILING DATE: 1997-02-19

/ NUMBER OF SEQ ID NOS: 6

/ SEQ ID NO 1

/ SOFTWARE: Patentin Ver. 2.1

/ LENGTH: 266

/ TYPE: PRT

/ ORGANISM: Human papillomavirus type 16

us-09-367-309A-1

Query Match 100.0%; Score 125; DB 9; Length 266;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNP₂A₁VCDKCLKFYSKIS₁Y 22

Db 62 RDGNP₂A₁VCDKCLKFYSKIS₁Y 83

RESULT 5

US-10-000-903-4

/ Sequence 4, Application US/10000903

/ Publication No. US20020182221A1

/ GENERAL INFORMATION:

/ APPLICANT: Bruck, Claudine

/ APPLICANT: Cabezon, Silvia, Teresa

/ APPLICANT: Delisse, Anne-Marie Eva Fernande

/ APPLICANT: Gerard, Catherine Marie Ghislaine

/ APPLICANT: Lombardo-Bencheikh, Angela

/ TITLE OF INVENTION: Vaccine

/ FILE REFERENCE: B45107

CURRENT APPLICATION NUMBER: US/10/000,903

PRIOR APPLICATION NUMBER: PCT/EP98/05285

CURRENT FILING DATE: 2001-10-01

PRIOR FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 273

TYPE: PRT

ORGANISM: Homo sapien

us-10-000-903-4

Query Match 100.0%; Score 125; DB 13; Length 273;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNP₂A₁VCDKCLKFYSKIS₁Y 22

Db 168 RDGNP₂A₁VCDKCLKFYSKIS₁Y 189

RESULT 6

US-10-000-903-10

/ Sequence 10, Application US/10000903

/ Publication No. US20020182221A1

/ GENERAL INFORMATION:

/ APPLICANT: Bruck, Claudine

/ APPLICANT: Cabezon, Silvia, Teresa

/ APPLICANT: Delisse, Anne-Marie Eva Fernande

/ APPLICANT: Gerard, Catherine Marie Ghislaine

/ APPLICANT: Lombardo-Bencheikh, Angela

/ TITLE OF INVENTION: Vaccine

/ FILE REFERENCE: B45107

CURRENT APPLICATION NUMBER: US/10/000,903

CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: PCT/EP98/05285

PRIOR FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: GB 9717953.5
 PRIOR FILING DATE: 1997-08-22
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 10
 LENGTH: 292
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-000-903-10

Query Match Score 125; DB 13; Length 292;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 22; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 22
 Db 187 RDGNYAVCDKCLKFYSKISEY 208

RESULT 8
 US-10-000-903-14

Query Match Score 125; DB 13; Length 371;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 22
 Db 168 RDGNYAVCDKCLKFYSKISEY 189

RESULT 9
 US-10-476-570-11

Sequence 11, Application US/10476570
 Publication No. US20040170644A1

GENERAL INFORMATION:
 APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 MAILLERE, Bernard
 BOURGAULT-VILLADA, Isabelle
 POUILLY-MORATILLE, Sandra
 POULEY, Jean-Gerard
 GUILLET, Catherine Marie Ghislaine
 Gérard, Catherine Marie Ghislaine
 Lombardo-Bencheikh, Angela
 TITLE OF INVENTION: Mixture of Peptides derived from E6 and/or E7
 TITLE OF INVENTION: Papillomavirus proteins and uses thereof
 FILE REFERENCE: 45636-5071-US
 CURRENT APPLICATION NUMBER: US/10/476,570
 CURRENT FILING DATE: 2003-11-04
 PRIOR APPLICATION NUMBER: PCT/FR02/01533
 PRIOR FILING DATE: 2003-05-03
 PRIOR APPLICATION NUMBER: FR 01 05980
 PRIOR FILING DATE: 2001-05-04
 NUMBER OF SEQ ID NOS: 63
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 11
 LENGTH: 20
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:
 OTHER INFORMATION: Description of the artificial sequence: Peptide E6 61-80
 US-10-476-570-11

Query Match Score 109; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 19
 Db 2 RDGNYAVCDKCLKFYSKISEY 20

RESULT 10
 US-10-472-724-6

Sequence 6, Application US/10472724
 Publication No. US20040171806A1

GENERAL INFORMATION:
 APPLICANT: Cid-Arregui, Angel
 Zurhausen, Harald
 TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 FILE REFERENCE: 4121-154
 CURRENT APPLICATION NUMBER: US/10/472,724
 CURRENT FILING DATE: 2003-09-17
 PRIOR APPLICATION NUMBER: PCT/EP02/03271
 PRIOR FILING DATE: 2002-01-22
 PRIOR APPLICATION NUMBER: EP 01107271.7
 PRIOR FILING DATE: 2001-03-23
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 6

Query Match Score 125; DB 13; Length 390;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 22; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 22
 Db 187 RDGNYAVCDKCLKFYSKISEY 208

LENGTH: 172
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Construct
 US-10-472-724-6

Query Match Score 71; DB 16; Length 172;
 Best Local Similarity 57.1%; Fred. No. 0.015; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RDGNPAVCDKLFYSKISE 21
 Db 63 RDSIPHACHRCIDFYSRRE 83

RESULT 11
 US-10-000-903-21
 Sequence 21, Application US/10000903
 Publication No. US20020182221A1
 GENERAL INFORMATION:
 APPLICANT: Bruck, Claudine
 APPLICANT: Cabezon Silva, Teresa
 APPLICANT: Delisse, Anne-Marie Eva Fernande
 APPLICANT: Gerard, Catherine Marie Ghislaine
 APPLICANT: Lombardo-Bancheikh, Angela
 TITLE OF INVENTION: Vaccine
 CURRENT APPLICATION NUMBER: US/10/0000,903
 CURRENT FILING DATE: 2001-10-01
 PRIOR APPLICATION NUMBER: PCT/EP98/05285
 PRIOR FILING DATE: 1998-08-17
 PRIOR APPLICATION NUMBER: GB 9717953.5
 PRIOR FILING DATE: 1997-08-22
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 21
 LENGTH: 278

TYPE: PRT
 ORGANISM: Homo sapien
 US-10-000-903-21

Query Match Score 71; DB 13; Length 278;
 Best Local Similarity 57.1%; Fred. No. 0.024; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RDGNPAVCDKLFYSKISE 21
 Db 168 RDSIPHACHRCIDFYSRRE 188

RESULT 12
 US-10-000-903-23
 Sequence 23, Application US/10000903
 Publication No. US20020182221A1
 GENERAL INFORMATION:
 APPLICANT: Bruck, Claudine
 APPLICANT: Cabezon Silva, Teresa
 APPLICANT: Delisse, Anne-Marie Eva Fernande
 APPLICANT: Gerard, Catherine Marie Ghislaine
 APPLICANT: Lombardo-Bancheikh, Angela
 TITLE OF INVENTION: Vaccine
 FILE REFERENCE: B45107
 CURRENT APPLICATION NUMBER: US/10/0000,903
 CURRENT FILING DATE: 1998-08-17
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 23
 LENGTH: 383

TYPE: PRT
 ORGANISM: Homo sapien
 US-10-000-903-23

Query Match Score 71; DB 13; Length 383;
 Best Local Similarity 57.1%; Fred. No. 0.033; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RDGNPAVCDKLFYSKISE 21
 Db 168 RDSIPHACHRCIDFYSRRE 188

RESULT 13
 US-08-344-824-237
 Sequence 237, Application US/08344824
 Publication No. US20030152580A1
 GENERAL INFORMATION:
 APPLICANT: SETTE, Alessandro
 APPLICANT: SIDNEY, John
 TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
 NUMBER OF SEQUENCES: 399
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Stewart Street Tower, 20th
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPETITOR: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,824
 FILING DATE: 23-NOV-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/278,634
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14137-80-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 237:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-344-824-237

Query Match Score 61; DB 8; Length 10;
 Best Local Similarity 100.0%; Fred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NPYAVCDKCL 13
 Db 1 NPYAVCDKCL 10

RESULT 14
 US-08-344-824-346
 Sequence 346, Application US/08344824
 Publication No. US20030152580A1
 GENERAL INFORMATION:
 APPLICANT: SETTE, Alessandro

APPLICANT: SIDNEY, John
 TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
 NUMBER OF SEQUENCES: 399
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Stewart Street Tower, 20th
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,824
 FILING DATE: 23-NOV-1994
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/278,634
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14137-80-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-1043

INFORMATION FOR SEC ID NO: 346:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-344-824-346

RESULT 15
 US-10-424-599-252512
 Query Match Score 56; DB 15; Length 462;
 Best Local Similarity 47.4%; Prod. No. 6.9;
 Matches 3; Conservative 3; Mismatches 7;
 Indels 0; Gaps 0;

Qy 3 GNPYAVCDKLCIKEYSKISSE 21
 Db 227 GKPYRVCDSCFVKLNKVAE 245

Search completed: November 22, 2004, 20:48:54
 Job time : 99.5 secs

US-10-424-599-252512
 Query Match Score 44.8%;
 Best Local Similarity 47.4%;
 Matches 3; Conservative 3; Mismatches 7;
 Indels 0; Gaps 0;
 Qy 3 GNPYAVCDKLCIKEYSKISSE 21
 Db 227 GKPYRVCDSCFVKLNKVAE 245

Computer readable form:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,824
 FILING DATE: 23-NOV-1994
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/278,634
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14137-80-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-1043
 INFORMATION FOR SEC ID NO: 346:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-344-824-346

Query Match Score 45.6%; DB 8; Length 9;
 Best Local Similarity 100.0%; Prod. No. 1.4e+06;
 Matches 0; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 4 NPYAVCDKC 12
 Db 1 NPYAVCDKC 9

RESULT 15
 US-10-424-599-252512
 Sequence 25512, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovacic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 EFILE REFERENCE: 38-21-(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 252512
 LENGTH: 462
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1) . (462)
 OTHER INFORMATION: unsure at all Xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_70045C.1.pep

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:20:21 ; Search time 27.5 Seconds
(without alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued_Patents_AA:
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2: /cgnd_6_ptodata1/iaa/5B_COMBO_pep:**
3: /cgnd_6_ptodata1/iaa/6A_COMBO_pep:**
4: /cgnd_6_ptodata1/iaa/6B_COMBO_pep:**
5: /cgnd_6_ptodata1/iaa/PC7US_COMBO_pep:**
6: /cgnd_6_ptodata1/iaa/backfile1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	125	100.0	158	4	US-09-980-523A-2	Sequence 2, Appli
2	125	100.0	162	1	US-08-316-239B-3	Sequence 3, Appli
3	125	100.0	162	1	US-08-316-239B-4	Sequence 4, Appli
4	125	100.0	172	3	US-08-860-165-14	Sequence 14, Appli
5	125	100.0	172	3	US-09-359-382-14	Sequence 14, Appli
6	125	100.0	266	3	US-08-860-165-10	Sequence 10, Appli
7	125	100.0	266	3	US-09-359-382-10	Sequence 10, Appli
8	125	100.0	266	4	US-09-367-309A-1	Sequence 1, Appli
9	125	100.0	273	3	US-09-485-885-4	Sequence 4, Appli
10	125	100.0	292	3	US-09-485-885-10	Sequence 10, Appli
11	125	100.0	371	3	US-09-485-885-6	Sequence 6, Appli
12	125	100.0	390	3	US-09-485-885-14	Sequence 14, Appli
13	125	91.2	172	3	US-08-860-165-12	Sequence 12, Appli
14	114	91.2	172	3	US-08-359-382-12	Sequence 12, Appli
15	103	82.4	20	2	US-08-934-915-162	Sequence 162, Appli
16	71	56.8	158	2	US-08-247-904B-10	Sequence 10, Appli
17	71	56.8	158	3	US-08-67-42A-19	Sequence 19, Appli
18	71	56.8	271	1	US-08-117-083-14	Sequence 14, Appli
19	71	56.8	278	3	US-09-485-885-21	Sequence 21, Appli
20	71	56.8	368	3	US-09-000-094-20	Sequence 20, Appli
21	71	56.8	368	4	US-10-011-749-10	Sequence 20, Appli
22	71	56.8	368	4	US-09-000-094-20	Sequence 20, Appli
23	71	56.8	375	3	US-09-000-094-22	Sequence 22, Appli
24	71	56.8	375	4	US-10-011-749-12	Sequence 22, Appli
25	71	56.8	383	3	US-09-485-885-23	Sequence 23, Appli
26	71	56.8	465	3	US-09-000-094-24	Sequence 24, Appli
27	71	56.8	465	4	US-09-000-094-24	Sequence 24, Appli

RESULT 1
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 673783
; GENERAL INFORMATION:
; APPLICANT: BOUFGAULT, VILLEADA, ISABELLE
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYEPITOPE PROTEIN FRAGMENTS OF THE E6 AND E7 PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO01 A0 INS
; CURRENT APPLICATION NUMBER: US/09-980-523A
; PRIORITY APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; SOFTWARE: Patentin Ver. 2.1
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO: 2
; LENGTH: 158
; TYPE: PT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 125; DB 4; Length 158;
Best Local Similarity 100.0%; Prod. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RDGNYAVIDKCLXFKYSKISEY 22
Db 62 RDGNYAVIDKCLXFKYSKISEY 83

RESULT 2
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Partmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for Distinguishing a Subset of HPV that is Associated with an Increased Risk of Developing Cervical Dysplasia and Cervical Cancer
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an Increased Risk of Developing Cervical Dysplasia and Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

TELECOMMUNICATION INFORMATION:
 ADDRESSSEE: Jegtiani & Associates
 STREET: 6126 Rocky Way Court
 CITY: Centreville
 STATE: VA
 COUNTRY: USA
 ZIP: 20120-3400
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/316,239B
 FILING DATE: 30-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jegtiani, Ajay A.
 REGISTRATION NUMBER: 35,205
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 803-9387
 TELEX/FAX: (703) 817-9453
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 162 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 -08-316-239B-3

RESULT 3
 Query Match 100.0%; Score 125; DB 1; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 /
 1 RDGNPYAVCDKCLKFYSKISEY 22
 62 RDGNPYAVCDKCLKFYSKISEY 83

Query Match 100.0%; Score 125; DB 1; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 /
 1 RDGNPYAVCDKCLKFYSKISEY 22
 62 RDGNPYAVCDKCLKFYSKISEY 83

US-08-316-239B-4

RESULT 4
 US-08-880-165-14
 Sequence 14, Application US/08860165A
 ; Patent No. 6004557
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 17227/13.0
 ; CURRENT APPLICATION NUMBER: US/08/860,165A
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868
 ; EARLIER FILING DATE: 1997-09-22
 ; EARLIER APPLICATION NUMBER: AU PN0157
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

Query Match 100.0%; Score 125; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-960-165-14

RESULT 5
 US-09-359-382-14
 Sequence 14, Application US/09359382
 ; Patent No. 6303397
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 01727/0148
 ; CURRENT APPLICATION NUMBER: US/09/359,382
 ; CURRENT FILING DATE: 1999-07-23
 ; EARLIER APPLICATION NUMBER: US 08/860,165
 ; EARLIER FILING DATE: 1997-05-22

Query Match 100.0%; Score 125; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 131 RDGNPYAVCDKCLKFYSKISEY 152

US-09-359-382-14

RESULT 6
 US-09-359-382-14
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/316,239B
 FILING DATE: 30-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jegtiani, Ajay A.
 REGISTRATION NUMBER: 35,205
 REFERENCE DOCKET NUMBER: UNME-0001

; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94

; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 14

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-09-359-382-14

Query Match 100.0%; Score 125; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYSKISEY 22

Db 131 RDGNPYAVCDKCLKFYSKISEY 152

RESULT 6

US-08-860-165-10

; Sequence 10, Application US/08860165A

; Patent No. 6004557

; GENERAL INFORMATION:

; APPLICANT: COX, John

; ATTORNEY: Edwards, Stirling John

; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE-OF-INVENTION: VARIANTS-OF-HUMAN-PAPILLOMA-VIRUS-ANTIGENS

; FILE REFERENCE: 17227/130

; CURRENT FILING DATE: 1997-09-22

; CURRENT APPLICATION NUMBER: US/08/860,165A

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; LENGTH: 165-10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-10

Query Match 100.0%; Score 125; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGAPYAVCDKCLKFYSKISEY 22

Db 62 RDGNPYAVCDKCLKFYSKISEY 83

RESULT 7

US-09-359-382-10

; Sequence 10, Application US/09359382

; Patent No. 6306397

; GENERAL INFORMATION:

; APPLICANT: COX, John

; ATTORNEY: Edwards, Stirling John

; APPLICANT: COX, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 017227/0148

; CURRENT FILING DATE: 1999-07-23

; CURRENT APPLICATION NUMBER: US/09/359,382

; EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: US/08/860,165

; EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ_for_Windows_Version_3.0

; SEQ ID NO: 4

RESULT 8

US-09-367-309A-1

; Sequence 1, Application US/09367309A

; Patent No. 6428807

; GENERAL INFORMATION:

; APPLICANT: MACPARLAN, RODERICK I.

; ATTORNEY: MALLAROS, JIM

; TITLE-OF-INVENTION: CHELLATING-IMMUNOSTIMULATING-COMPLEXES

; FILE REFERENCE: 017227/0149

; CURRENT FILING DATE: 1999-07-31

; CURRENT APPLICATION NUMBER: US/09/367-309A

; PRIOR APPLICATION NUMBER: PCT/AU98/00080

; PRIOR FILING DATE: 1998-02-13

; PRIOR FILING DATE: 1997-07-19

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 1

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-09-367-309A-1

Query Match 100.0%; Score 125; DB 4; Length 266;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGPNPVAVCDCKLKEYSKISEY 22

Db 62 RDGPNPVAVCDCKLKEYSKISEY 83

RESULT 9

US-09-485-865-4

; Sequence 4, Application US/09485865

; Patent No. 634224

; GENERAL INFORMATION:

; APPLICANT: Bruck, Claudine

; ATTORNEY: Cabezon Silvia, Teresa

; APPLICANT: Delisse, Anne-Marie Eva Fernande

; APPLICANT: Gerard, Catherine Marie Ghislaine

; APPLICANT: Lombardo-Bencheikh, Angels

; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: B45107

; CURRENT APPLICATION NUMBER: US/09/485,885

; CURRENT FILING DATE: 2000-02-18

; CURRENT APPLICATION NUMBER: PCT/EP98/05285

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: GB 9717953.5

; PRIOR FILING DATE: 1997-08-22

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ_for_Windows_Version_3.0

; SEQ ID NO: 4

RESULT 11
US-09-485-885-6
Query Match 100.0%; Score 125; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RDGNPVAVCDCRCLKFYSKISY 22
Db 168 RDGNPVAVCDCRCLKFYSKISY 189

RESULT 12
US-09-485-885-14
Sequence 14, Application US/09485885
Patent No. 634224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
Cabezon-Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485, 885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/BP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 10
LENGTH: 292
TYPE: PRT
ORGANISM: Homo sapien
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 10
LENGTH: 292
TYPE: PRT
ORGANISM: Homo sapien
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 6
LENGTH: 371
TYPE: PRT
ORGANISM: Homo sapien

RESULT 13
US-08-860-165-12
Sequence 12, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
COX, John Cooper
WEBB, Elizabeth Ann
FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 112227130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00866
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 12
LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Other Information: Description of Artificial Sequence: Gene Fusion
OTHER INFORMATION: US-08-860-165-12

Query Match 91.2%; Score 114; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred. No. 7 8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 3 GNPYAVCDKCLKFYSKISY 22
 DB 2 GNPYAVCDKCLKFYSKISY 21

RESULT 14 US-09-359-3B2-12

Sequence 12. Application US/09359382
 Patent No. 6306597
 GENERAL INFORMATION:
 APPLICANT: COX, John Cooper
 APPLICANT: WEBB, Elizabeth Ann
 APPLICANT: FRAZER, Ian
 TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 FILE REFERENCE: 11722/01/48
 CURRENT FILING DATE: 1999-07-23 US/09/359,382
 EARLIER APPLICATION NUMBER: US 08/860,165
 EARLIER FILING DATE: 1997-09-12
 EARLIER APPLICATION NUMBER: PCT/AU95/00868
 EARLIER FILING DATE: 1995-12-20
 EARLIER APPLICATION NUMBER: AU PN0157/94
 EARLIER FILING DATE: 1994-12-20
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 12
 LENGTH: 172
 TYPE: PRT
 ORGANISM: Human papillomavirus type 16
 US-09-359-3B2-12

Query Match 91.2%; Score 114; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred. No. 7 8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 3 GNPYAVCDKCLKFYSKISY 22
 DB 2 GNPYAVCDKCLKFYSKISY 21

RESULT 15 US-08-934-915-162

Sequence 162. Application US/08334915
 Patent No. 5932442
 GENERAL INFORMATION:
 APPLICANT: DILLNER, JOAKIM
 APPLICANT: DILLNER, LEONA
 APPLICANT: CHEUNG, HWEI-MING
 TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 PAPILLOVIRUS 1, 5, 6, 8,
 TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
 TITLE OF INVENTION: DIAGNOSTIC PURPOSES
 NUMBER OF SEQUENCES: 193
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MASON & ASSOCIATES, P.A.
 STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 CITY: CLEARWATER
 STATE: FLORIDA
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM-PC compatible
 OPERATING SYSTEM: Windows 3.0
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,915
 FILING DATE: 22-SEP-1997

Image blank (uspto)

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OM Protein - protein search, using sw model

Run on: November 22, 2004, 20:14:12 ; Search time 113.5 seconds
(without alignments)
69.533 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125

Sequence: 1 RDGNPYAVCDRCLRFYSKISEY 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:
1: geneseqP1980s: *
2: geneseqP1990s: *
3: geneseqP2000s: *
4: geneseqP2001s: *
5: geneseqP2002s: *
6: geneseqP2003as: *
7: geneseqP2003bs: *
8: geneseqP2004as: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	125	100.0	22	8	ADI34603	Adi34603 HPV 16 B6
2	125	100.0	151	6	AAO22640	Aao22640 HPV-16 pr
3	125	100.0	151	6	AAO22636	Aao22636 HPV prote
4	125	100.0	151	8	ADO44072	Ado44072 Amino aci
5	125	100.0	158	2	AAU22766	Aau22766 HPV E6 pe
6	125	100.0	158	4	AAY22462	Aay22462 Human Pap
7	125	100.0	158	4	AAB88420	Aab88420 Human Pap
8	125	100.0	158	7	ADF09515	Adf09515 Human Pap
9	125	100.0	158	8	ADL90078	Adl90078 Human Pap
10	125	100.0	162	2	AAW35741	AAw35741 Human Pap
11	125	100.0	162	2	AAW35742	AAw35742 Human Pap
12	125	100.0	171	5	AAU22922	Aau22922 Human Pap
13	125	100.0	172	2	AAR97563	Aar97563 Human Pap
14	125	100.0	180	7	ADF31985	Adf31985 Human Pap
15	125	100.0	188	2	AAR63865	Aar63865 HPV16 E6/
16	125	100.0	243	2	AAW993369	Aaw993369 Papilloma
17	125	100.0	248	8	ADO44060	Ado44060 Amino aci
18	125	100.0	248	8	ADO44066	Ado44066 Amino aci
19	125	100.0	263	2	AAR27725	Aar27725 HPV 16 E6
20	125	100.0	266	2	AAR97561	Aar97561 Human Pap
21	125	100.0	273	2	AAY25376	Aay25376 HPV fusio
22	125	100.0	273	2	AAY26332	Aay26332 Prot.DI/3
23	125	100.0	292	2	AAY25379	Aay25379 HPV fusio
24	125	100.0	292	2	AAY2635	Aay2635 CLYTA-E6-
25	125	100.0	371	2	AAY25377	Aay25377 HPV fusio

ALIGNMENTS

ALIGNMENTS

Aav25381

AAY02633

HPV fusio

AAT25381

CLYTA-E6

AAY02633

HPV-16 E6

AAY57808

Human pap

Aar97562

Amido aci

Add44062

Amino aci

Add44064

Amino aci

Add44068

Amino aci

Add44070

Amino aci

Add70252

Peptide d

Aav25381

HPV E6 re

Add44077

Amido aci

Aav25386

Peptide G

Aav29583

Peptide G

Aav29572

Peptide G

Aab1109

A polyepito

Add31017

Polyepito

Add44080

Amino aci

Aaw29587

Peptide G

Aav25381

HPV E6

(first entry)

XX

DB

HPV 16

early coding region derived peptide.

XX

CC cellular abnormalities selected from koilocytosis, hyperkeratosis,
 CC precancerous conditions encompassing intraepithelial lesions, high-grade
 CC dysplasias, invasive cancers and malignant cancers. The present sequence
 CC represents a specific example of a peptide derived from HPV 16 E6 early
 CC coding region.
 XX Sequence 22 AA;
 SQ Query Match 100.0%; Score 125; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC 1 RDGNPYAVCDKCLKFYSKISFY 22
 AC 1 RDGNPYAVCDKCLKFYSKISFY 22
 DT 15-MAY-2003 (first entry)
 DE HPV protein sequence, SEQ ID No 20.
 KW Cytostatic; Peptide therapy; immunotherapy; pre-; cancerous growth;
 KW cancer; human papilloma virus; cervix; cell-mediated immune response;
 KW HPV; HPV-16.
 XX Human papilloma virus.
 OS XX
 ID AAO22640 standard; protein; 151 AA.
 XX
 AC AAO22640;
 XX
 DT 15-MAY-2003 (first entry)
 XX HPV-16 protein sequence, SEQ ID No 27.
 XX Cytostatic; Peptide therapy; immunotherapy; pre-; cancerous growth;
 KW cancer; human papilloma virus; cervix; cell-mediated immune response;
 KW HPV; HPV-16.
 XX Human papilloma virus.
 OS XX
 PN WO2003008649-A1.
 XX
 PD 30-JAN-2003.
 XX 19-JUL-2002; 2002WO-US022198.
 PR 20-JUL-2001; 2001US-0306609P.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA Sastry KJ, Tortolero-Luna G, Follen N;
 PI XX
 DR WPI; 2003-239363/23.
 XX
 PT Determining a possible recurrence of a (pre-)cancerous growth in a
 PR patient infected with human papilloma virus (HPV), comprises incubating
 PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
 PR immune response.
 XX Disclosure; Page 125-126; 132pp; English.
 XX
 CC The invention relates to a novel method for determining the possibility
 CC of recurrence of a (pre-)cancerous growth in a patient infected with
 CC human papilloma virus (HPV) or suspected of being infected with HPV, and
 CC has or had a (pre-)cancerous growth on or around the cervix. The novel
 CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
 CC the patient, and assaying the sample for a cell-mediated immune response
 CC against the peptide. The method is useful for determining the possibility
 CC and preventing the recurrence of a (pre-)cancerous growth in a patient
 CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
 CC E7 peptides are useful in immunotherapy for the preventing or reducing
 CC the risk of development of (pre-)cancerous growths. This sequence
 CC represents an HPV protein of the invention.
 XX Sequence 151 AA;
 SQ Query Match 100.0%; Score 125; DB 6; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC 1 RDGNPYAVCDKCLKFYSKISFY 22
 AC 1 RDGNPYAVCDKCLKFYSKISFY 22
 DT 15-JUL-2004 (first entry)
 XX

XX Amino acid sequence of a wild type HPV16 E6 protein.

DE E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

KW Human papillomavirus type 16.

XX Synthetic.

OS WO2004030636-A2.

PN XX PD 02-APR-1992.

XX PF 26-SEP-1991; 91WO-US007081.

XX PR 26-SEP-1990; 90US-00588384.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;

XX DR WPI; 1992-132119/16.

XX Disclosure; Fig 7; 81pp; English.

XX Immunoactive peptide(s) derived from E6 or E7 region of HPV16 - and recombinant cells encoding them, useful in treatment and prophylaxis of cervical warts or cancer resulting from HPV infection.

XX PS The peptide is the sequence of the human papillomavirus HPV 16 E6 nucleoprotein. Peptides corresponding to regions (pref. epitopic regions) of HPV 16 E6 were synthesised by standard Merrifield synthesis. Examples of such peptides are E6 1-20, 8-20, 13-14 or 148-158. Compositions of these peptides, antibodies against the peptides, or recombinant cells containing the gene encoding the immunogenic peptides may be utilised in methods for inhibiting and treating HPV infection and tumour initiation and progression e.g. in the prevention or retardation of cervical warts and cervical carcinoma resulting from HPV infection. See also AR22167. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 158 AA;

Query Match Score 125; DB 2; Length 158;

Best Local Similarity 100.0%; Pred. No. 1.3e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNYAVCDKCLKFYSKISEY 22

Db 62 RDGNYAVCDKCLKFYSKISEY 83

XX RESULT 6

AY82462 standard; protein; 158 AA.

XX ID AAY82462;

XX AC AAY82462;

XX DT 30-JUN-2000 (first entry)

XX DE Human papillomavirus E6 protein containing two zinc finger motifs.

XX KW Chelated zinc finger; therapeutic; treatment; prophylaxis; MPV;

XX FN mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion; wart.

XX OS Human papillomavirus.

XX PH Key Location/Qualifiers

XX FT Misc-difference 37..73 /note= "forms a zinc finger motif"

XX FT Misc-difference 110..146 /note= "forms a zinc finger motif"

XX PN WO20014063-A1.

XX PD 16-MAR-2000.

XX PR 03-SEP-1999; 99WO-AU000724.

XX PR 04-SEP-1998; 98AU-00005733.

XX PR 15-JUN-1999; 99AU-00001645.

XX PN WO9205248-A.

XX RESULT 5

ID AAR22766 standard; peptide; 158 AA.

AC AAR22766;

XX DT 25-MAR-2003 (revised)

DT 21-SEP-1992 (first entry)

XX DE HPV E6 peptide.

XX KW Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.

XX OS Synthetic.

OS Homo sapiens.

XX PN WO9205248-A.

PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
 PA (HUGH-) HUGHES E J L.
 XX
 PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;
 XX
 DR WPI; 2000-256917/22.
 PT Polysulfide and dithionodisulfide agents, useful for the treatment or
 PT prophylaxis of diseases caused by mammalian papillomavirus, are
 PT disruptors of a chelated metal cation domain in an MPV gene encoded
 PT protein.
 XX
 Disclosure; Fig 1; 78pp; English.
 XX
 The present invention describes an agent used in the treatment or
 CC prophylaxis of a disease caused or exacerbated by MPV (mammalian
 CC papillomavirus) comprising a compound capable of reducing, inhibiting or
 CC otherwise decreasing the activity of a protein encoded by an MPV gene by
 CC facilitating disruption of a chelated metal cation domain present in the
 CC protein. An agent of the present invention can be used to treat cervical
 CC cancer or its HPV associated precursor lesions or other HPV associated
 CC cancers and/or warts. The present sequence represents a human
 CC papillomavirus B6 protein containing two zinc finger motifs, as given in
 CC the exemplification of the present invention
 XX Sequence 158 AA;

Query Match 100.0%; Score 125; DB 3; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy. 1 RDGNPYAVCDKCLKFYSKISEY 22
 Db 62 RDGNPYAVCDKCLKFYSKISEY 83

RESULT 7
 AAB98420 standard; protein; 158 AA.
 ID AAB98420
 XX AC AAB98420;
 XX DT 22-AUG-2001 (First entry)
 XX Human papillomavirus protein HPV16 E6.

DE Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
 XX KW epitope; T cell; identification; vaccine; infection; genital wart;
 KW neoplastic growth; antiviral.
 XX Human papillomavirus.
 OS WO200141799-A1.
 XX PN 11-DEC-2000; 2000WO-US031549.
 XX PR 10-DEC-1999; 99US-0172705P.
 XX PR 15-AUG-2000; 2000US-00641528.
 XX PA (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
 XX DR WPI; 2001-381497/40.

XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
 PT treating HPV infections.
 XX Disclosure; Page 20-21; 756pp; English.

XX PS The present invention describes an isolated prepared human papillomavirus
 CC

CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
 CC production. Peptides and corresponding nucleic acid compositions from the
 CC present invention are useful for stimulating an immune response to HPV by
 CC stimulating the production of CTL or HTL responses, specifically in the
 CC treatment or prophylaxis of HPV infection, in persons who have not
 CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
 CC can also be used in a tetramer staining assay to assess peripheral blood
 CC mononuclear cells for the presence of antigen-specific CTLs following
 CC exposure to pathogen or immunogen, and as reagents to evaluate immune
 CC recall responses or evaluate the efficacy of a vaccine. The vaccine
 CC compositions are useful for removing warts or treating HPV infections.
 CC The epitopes for inclusion in an epitope-base vaccine may be selected
 CC from conserved regions of viral or tumour-associated antigens, which
 CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
 CC that may be present in whole antigens can be avoided with the use of
 CC epitope-base vaccines. An additional advantage is the ability to combine
 CC selected epitopes (CTL and HTL) and to modify the composition of the
 CC epitopes achieving enhanced immunogenicity, the major benefit of the
 CC vaccine is that is safe and efficacious. AAB98427 to AAB98391 to AAB98391 to
 CC polypeptide sequences used in the exemplification of the present
 CC invention
 XX SQ Sequence 158 AA;

Query Match 100.0%; Score 125; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-01;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy. 1 RDGNPYAVCDKCLKFYSKISEY 22
 Db 62 RDGNPYAVCDKCLKFYSKISEY 83

RESULT 8
 ADF09515 standard; protein; 158 AA.
 ID ADF09515
 XX AC ADF09515;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human papillomavirus 16 E6 SEQ ID NO:16.
 XX KW human; protein-protein interaction; virucide; cytostatic; vaccine;
 XX KW human papilloma virus; HPV; cancer.
 XX OS Human papillomavirus.
 XX PN WO2003068940-A2.
 XX PD 21-AUG-2003.
 XX PF 14-FEB-2003; 2003WO-US004594.
 XX PR 14-FEB-2002; 2002US-0356911P.
 XX PA (CURA- CURAGEN CORP.
 XX PA (HOFF) HOFFMANN LA ROCHE INC.
 XX PI Jackson A, Ooi CE, Lewin DA, Cuthill S;
 XX DR WPI; 2003-689668/65.
 XX N-PSDB; ADF09607.

PT New purified complex comprising a first polypeptide and a second
 PT polypeptide, useful for identifying agents for treating/preventing a
 PT condition involving altered level of the complex e.g. human papilloma
 PT virus infection, or cancer.
 XX PS Example 3; SEQ ID NO 16; 156pp; English.
 XX CC The invention relates to a novel purified complex comprising a first
 CC polypeptide and a second polypeptide, where the polypeptides comprise

defined amino acid sequences listed in the specification, and where the first polypeptide binds to the second polypeptide. A complex of the invention has virucide and cytotoxic activity, and may have a use as a vaccine. The complex is useful for identifying agents for treating or preventing conditions involving altered level of the complex, e.g., human papilloma virus (HPV) infection, or cancer. The compositions, antibodies, vectors and methods are useful for treating such diseases.

The sequences shown in ADF09500-ADF09583 represent proteins of the invention.

SQ Sequence 158 AA;

Query Match 100.0%; Score 125; DB 7; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 RDGNNPYAVCDKCLKFKYSKISEY 22

DY 62 RDGNNPYAVCDKCLKFKYSKISEY 83

RESULT 9
ADL90078

ID ADL90078 standard; protein; 158 AA.

AC ADL90078;
XX DT 17-JUN-2004 (First entry)

XX DE Human papillomavirus 16-E6 protein, SEQ ID 18.

XX KW Immune response; immunoglobulin; Ig; E6.

XX OS Human papillomavirus.

XX PN WO00402049-A2.

XX PD 01-APR-2004.

XX PF 18-SEP-2003; 2003NC0-US030188.

XX PR 20-SEP-2002; 2002US0-0412219P.

XX PR 14-MAR-2003; 2003NC0-US007995.

PA (ASTR-) ASTRAL INC.

XX Bot A, Wang L, Smith D, Phillips B;

XX WPI; 2004-295415/27.

XX Generating an immune response to an antigen, useful for generating desired T cell responses comprising administering an immunoglobulin having one peptide epitope of the antigen attached to the immunoglobulin.

XX Disclosure; Fig 1G; 154PP; English.

XX The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. The present sequence is an antigen sequence, used to illustrate the invention.

XX SQ Sequence 158 AA;

Query Match 100.0%; Score 125; DB 8; Length 158;

Best Local Similarity 100.0%; Pred. No. 1.3e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNNPYAVCDKCLKFKYSKISEY 22

DB 62 RDGNNPYAVCDKCLKFKYSKISEY 83

RESULT 10
AAW35741 standard; protein; 162 AA.
ID AAW35741.
AC AAW35741;
XX DT 25-MAR-2003 (revised)
DT 16-FEB-1998 (first entry)
XX DE Human papillomavirus type 16 E6 protein.

XX KW Complete genome; circular; human papillomavirus type 16; HPV16 E6; cervical dysplasia; cervical cancer; cervical smear.

XX OS Human papillomavirus type 16.

XX PT Key Location/Qualifiers
PH Misc-difference 90 /note= "Mutated to Val in the variant"
PT Misc-difference 159 /note= "End of protein sequence even though 3 amino acid residues are given following ori"
PT PT=

XX XX US5679509-A.

XX DN 21-OCT-1997.
XX XX 30-SEP-1994;
XX PF 28-SEP-1993;
XX PR 04-UNYNE) UNIV NEW MEXICO STATE.
XX PA (UYNE) UNIV NEW MEXICO STATE.

XX PT Wheeler CM, Carpenter CA;
XX FI XX WPI; 1997-525714/48.
XX DR N-PSDB; AAT94723.

XX PT Evaluating risk of cervical dysplasia or cervical cancer - by detecting variant form of human papillomavirus 16.

XX PT XX Claim 7; Col 23-24; 33pp; English.

XX CC Methods have been developed for distinguishing a subset of human papillomavirus (HPV) that is associated with an increased risk of developing cervical dysplasia or cervical cancer. The methods involve:

CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the sample and determining if the base at position 350 of the E6 gene (see AAT94723 and AAT94724 for comparison) is T or G, where the presence of G at position 350 is associated with an increased risk of developing cervical dysplasia or cervical cancer; and (2) preparing a cervical sample to expose any HPV-16 E6 protein in the sample and determining if the amino acid at position 83 of the protein (see position 90 in AAT94723 and AAT94724 for comparison) is Val or Leu, where the presence of Val at position 83 that is associated with an increased risk of developing cervical dysplasia or cervical cancer. The present sequence represents the reference protein sequence for HPV-16 E6. The 350G variant correlates well with Pap scores: 350:350G ratios among 45 HPV16 samples were 10.4 for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CRN III; 0.3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 162 AA;

Query Match 100.0%; Score 125; DB 2; Length 162;

Best Local Similarity 100.0%; Pred. No. 1.4e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNNPYAVCDKCLKFKYSKISEY 22

DB 62 RDGNNPYAVCDKCLKFKYSKISEY 83

RESULT 11
 AAW35742 standard; protein; 162 AA.
 ID AAW35742
 XX
 AC AAW35742;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-FEB-1998 (first entry)
 DE Human papillomavirus type 16 E6 protein variant.
 XXX
 KW Complete genome; circular; human papillomavirus type 16; HPV16 E6;
 KW cervical dysplasia; cervical cancer; cervical smear.
 XX
 OS Human papillomavirus type 16.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 90
 FT /note= "Mutated from Leu in the reference sequence
 FT (AAW35741)"
 FT Misc-difference 159
 FT /note= "End of protein sequence even though 3 amino acid
 FT residues are given following on"
 XX
 US5679509-A.
 PN PR
 XX PD 21-OCT-1997.
 XX PF 30-SEP-1994; 94US-00316239.
 XX PR 28-SEP-1993; 93US-00127906.
 XX PA (UYNE-) UNIV NEW MEXICO STATE.
 XX PI Wheeler CM, Parmenter CA;
 XX DR WPI; 1997-225714/48.
 DR N-PSDB; AAI94742.
 XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting
 PT PT variant form of human papilloma virus 16.
 XX Claim 7: Col 23-26; 33pp; English.
 XX Methods have been developed for distinguishing a subset of human
 CC papilloma virus (HPV) that is associated with an increased risk of
 CC developing cervical dysplasia or cervical cancer. The methods involve:
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the
 CC sample and determining if the base at position 350 of the E6 gene (see
 PS AAT94123 and AAT94724 for comparison) is T or G, where the presence of G
 XX at position 350 is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical
 CC sample to expose any HPV-16 E6 protein in the sample and determining if
 CC the amino acid at position 83 of the protein (see position 30 in AAW35741
 CC and AAW35742 for comparison) is Val or Leu, where the presence of Val at
 CC position 83 that is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer. The present sequence represents
 CC the variant protein sequence for HPV-16 E6. The 350G variant correlates
 CC well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4
 CC for negative Pap scores; 4:2 for CIN I; 1:6 for CIN II; 2:9 for
 CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct P# field.)
 XX Sequence 162 AA;

RESULT 12
 AAO22922 standard; protein; 171 AA.
 ID AAO22922
 XX
 AC AAO22922;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human Papillomavirus-16 (HPV16) E6ET-protein sequence.
 XX
 KW Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
 KW fusion partner; immunogenicity; HPV infection; neoplasm; HPV16;
 KW human papillomavirus-16; E6ET-sequence.
 XX
 OS Human papillomavirus.
 XX
 PN EP1243655-A1.
 XX
 PD 25-SEP-2002.
 XX
 PF 23-MAR-2001; 2001EP-00107271.
 XX
 PR 23-MAR-2001; 2001EP-00107271.
 XX
 PA (DEBKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Cid-Arregui A, Zur Hausen H;
 XX
 WP1; 2002-724952/79.
 DR N-PSDB; ARI53420
 XX
 A new DNA sequence encoding a fusion protein comprising a mutagenized HPV
 PR (human papillomavirus) E6 Or E7 coding sequence and a sequence encoding a
 PR highly immunogenic fusion partner is useful to vaccinate against HPV
 XX
 Disclosure; Fig 2; 34pp; English.

CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion
 CC protein of HPV, where at least 20% of the original codons are replaced by
 CC codons which lead to enhanced translation in a mammalian cell, containing
 CC a mutation which results in production of a truncated non-functional
 CC protein, and encoding a highly immunogenic polypeptide fusion partner
 CC capable of enhancing immunogenicity of the E6 or E7 protein in the
 CC mammalian host. The invention is used as a vaccine for the prevention or
 CC treatment of an HPV infection or a neoplasm associated with HPV
 CC infection. This sequence represents the human papillomavirus-16 (HPV16)
 CC E6ET-protein sequence of the invention.

XX Sequence 171 AA;

Query Match Score 125; DB 5; Length 171;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYSKISEY 22
 Ds 67 RDGNPYAVCDKCLKFYSKISEY 88

RESULT 13
 AAR97563 standard; protein; 172 AA.
 ID AAR97563
 XX
 AC AAR97563;
 XX
 DT 27-AUG-2003 (revised)
 DT 11-JAN-1997 (first entry)
 XX
 DE Human papilloma virus E6/E7 protein variant.
 XX
 Human Papilloma virus; E6; E7; deletion mutant; HPV; immune response;

Qy 1 RDGNPYAVCDKCLKFYSKISEY 22
 Ds 62 RDGNPYAVCDKCLKFYSKISEY 83

KW humoral immune response; cellular immune response; vaccine.
 XX
 OS Human Papillomavirus.
 XX
 PN WO9619496-A1.

XX PD 27-JUN-1996.
 XX PF 20-DEC-1995; 95WO-AU0000865.
 XX PR 20-DEC-1994; 94AU-00000157.
 XX PA (CSLC-) CSL LTD.
 PA (TQU) UNIV QUEENSLAND.
 XX Edwards SJ, Cox J, Webb EA, Frazer I;
 XX PI WPI: 1996-30518/31.
 DR N-PSDB; AT311835.

XX Vaccine variants of human papilloma virus antigens - contain variants of E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a deletion mutant comprising at least half, and preferably two-thirds of full length E6 or E7 protein starting from the N- or C-terminal, or is a full length E6 moiety fused to a full length E7 moiety. The variant optionally has a linkage moiety and foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This sequence is a fusion protein of the C-terminal end of E7 and the N-terminal end of E6. (Updated on 27-AUG-2003 to correct OS field.)

Sequence 172 AA;

Query Match Score 125; DB 2; Length 172;

Best Local Similarity 100.0%; Prod. No. 1_5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Claim 8; SEQ ID NO 2; 16pp; Chinese.

The present invention relates to human papillomavirus E6/E7 fusion gene, its preparing process, the process for configuring the efficient expression carrier containing the gene and resultant expression carrier, the fusion protein prepared from the gene, and the application of the fusion gene and expression protein to medical science and medicine to treat cervix cancer are disclosed. The present sequence represents the human papillomavirus fusion gene.

Sequence 180 AA;

Query Match Score 125; DB 7; Length 180;
 Best Local Similarity 100.0%; Prod. No. 1_5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFSKSEY 22
 Db 62 RDGNPYAVCDKCLKFSKSEY 83

RESULT 15 AAR63865 standard; protein; 188 AA.

ID AAR63865 DT 16-OCT-2003 (revised)
 XX AC AAR63865; DT 25-MAR-2003 (revised)
 XX DE HPV16 E6/E7 proteins. DT 28-JUN-1995 (first entry)

XX HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia; cervix cancer.

XX OS Human papillomavirus; strain 16.

XX PH Key Protein 1:i:158 /label= E6_protein
 FT Protein 159 ; 188
 FT /label= E7_protein

XX PN WO9422934-A2.

XX PD 24-NOV-1994.
 XX PP 06-MAY-1994; 94WO-US005085.
 XX PR 06-MAY-1993; 93US-00058920.

XX PA (BAXT) BAXTER DIAGNOSTICS INC.

XX PI Brown JT;
 XX DR WPI: 1995-006821/01.
 XX DR P-PSDB; AAQ75470.

XX PR Human papilloma virus detection assay - by amplification using self sustained sequence replication and hybridisation with a detector probe.

XX Disclosure; Page 24-26; 79pp; English.

CC The sequences of the E6 and E7 polypeptide-encoding regions of human

PI Zhao Q;
 XX WPI: 2003-258260/26.
 DR N-PSDB; ADF31984.
 XX Human papillomavirus E6/E7 fusion gene and its efficient expression carrier and fusion protein vaccine.

PT
 XX
 PS
 XX
 CC The present invention relates to human papillomavirus E6/E7 fusion gene, its preparing process, the process for configuring the efficient expression carrier containing the gene and resultant expression carrier, the fusion protein prepared from the gene, and the application of the fusion gene and expression protein to medical science and medicine to treat cervix cancer are disclosed. The present sequence represents the human papillomavirus fusion gene.

XX Sequence 180 AA;

Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 1_5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFSKSEY 22
 Db 62 RDGNPYAVCDKCLKFSKSEY 83

RESULT 15 AAR63865 standard; protein; 188 AA.

ID AAR63865 DT 16-OCT-2003 (revised)
 XX AC AAR63865; DT 25-MAR-2003 (revised)
 XX DE HPV16 E6/E7 proteins. DT 28-JUN-1995 (first entry)

XX HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia; cervix cancer.

XX OS Human papillomavirus; strain 16.

XX PH Key Protein 1:i:158 /label= E6_protein
 FT Protein 159 ; 188
 FT /label= E7_protein

XX PN WO9422934-A2.

XX PD 24-NOV-1994.
 XX PP 06-MAY-1994; 94WO-US005085.
 XX PR 06-MAY-1993; 93US-00058920.

XX PA (BAXT) BAXTER DIAGNOSTICS INC.

XX PI Brown JT;

XX DR WPI: 1995-006821/01.

XX PR Human papilloma virus detection assay - by amplification using self sustained sequence replication and hybridisation with a detector probe.

XX Disclosure; Page 24-26; 79pp; English.

CC The sequences of the E6 and E7 polypeptide-encoding regions of human

CC Papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded
CC proteins in AAR63865-66, respectively. Probes and primers based on these
CC sequences were used for HPV infection diagnosis; expression of E6 and E7
CC is diagnostic for cervical cancer or pre-malignant states. (Updated on
CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
CC OS field)

XX

SQ Sequence 188 AA;

Query Match 100.0%; Score 125; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYSKISEY 22
D2 62 RDGNPYAVCDKCLKFYSKISEY 83

Search completed: November 22, 2004, 20:27:27
Job time : 115.5 secs

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OM Protein - protein search, using sw model

Run on: November 22, 2004, 20:14:12 ; Search time 113.5 Seconds
(without alignments)

69.533 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFGSRIRLHRYSVYGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_GenSeq_23Sep04:
 1: genSeqP1980s:**
 2: genSeqP1990s:**
 3: genSeqP2000s:**
 4: genSeqP2001s:**
 5: genSeqP2002s:**
 6: genSeqP2003s:**
 7: genSeqP2003s:**
 8: genSeqP2004s:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	120	100.0	22	8 ADI34604	ADI34604 HPV 18 E6
2	111	92.5	32	2 AAR14751	Aar14751 Serotype
3	111	92.5	158	2 AAR63866	Aar63866 HPV18 E6/
4	111	92.5	158	2 AAR79656	Aar79656 HPV-18 E6
5	111	92.5	158	2 AAY39968	Aay39968 HPV-18 E6
6	111	92.5	158	3 AAB03176	Aab03176 HPV-18 E6
7	111	92.5	158	4 AAB98427	Aab98427 Human pap
8	111	92.5	8 ADL90077	Adl90077 Human pap	
9	111	92.5	158	8 ADO44074	Ado44074 Amino aci
10	111	92.5	172	5 AAO22924	Aao22924 Human pap
11	111	92.5	271	2 AAR27728	Aar27728 HPV 18 E6
12	111	92.5	278	2 AAY25385	Aay25385 HPV fusio
13	111	92.5	278	2 AAY05641	Aay05641 Prot.D/3
14	111	92.5	383	2 AAY25386	Aay25386 HPV fusio
15	111	92.5	383	2 AAY05642	Aay05642 Prot.D/3
16	96	80.0	158	4 AAB98440	Aab98440 Human pap
17	96	80.0	158	8 ADO44079	Ado44079 Amino aci
18	86	71.7	160	8 ADO44084	Ado44084 Amino aci
19	75	62.5	158	8 ADO44078	Ado44078 Amino aci
20	71	59.2	158	8 ADO44085	Ado44085 Amino aci
21	68	56.7	151	6 AAO22636	Aao22640 HPV-16 pr
22	68	56.7	151	6 AAO22636	Aao22636 HPV Prote
23	68	56.7	151	8 ADO44072	Ado44072 Amino aci
24	68	56.7	162	2 AAW35742	AAw35742 Human pap
25	68	56.7	248	8 ADO44062	Ado44062 Amino aci

ALIGNMENTS

RESULT 1	
ID	ADI34604 standard; peptide; 22 AA.
XX	
AC	ADI34604;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	HPV 18 E6 early coding region derived peptide.
XX	
HPV; E2; E6; E7; cancer; cellular abnormality.	
XX	
OS	Human papillomavirus.
XX	
PN	WO2004005469-A2.
XX	
PD	15-JAN-2004.
XX	
PR	02-JUL-2003; 2003WO-US020887.
XX	
PR	02-JUL-2002; 2002US-0394172P.
PR	01-JUL-2003; 2003US-00612818.
XX	
(IMPA-) IMPACT DIAGNOSTICS INC.	
PA	
XX	
PF	02-JUL-2003; 2003WO-US020887.
XX	
PR	02-JUL-2002; 2002US-0394172P.
PR	01-JUL-2003; 2003US-00612818.
XX	
PWPI	2004-142978/14.
XX	
New Peptides from the E2, E6 or E7 Proteins of human papillomavirus (HPV)	
PT	
PT	16 or 18, useful for detecting and/or diagnosing HPV-associated cellular
PT	abnormalities or cervical dysplasia or carcinoma.
XX	
XX	
Claim 4; SEQ ID NO 5; 31PP; English.	
XX	
CC	The invention relates to an isolated protein sequence or peptide from the
CC	E2, E6 or E7 early coding region of human papillomavirus (HPV) that is
CC	soluble in an aqueous medium, and characterized by a relative lack of
CC	tryptophan, methionine and cysteine residues, and a relative abundance of
CC	glycine and asparagine residues. The protein sequences can be used in a
CC	method for detecting or diagnosing cancer or cellular abnormalities. The
CC	method involves reacting a sample of body fluid or tissue likely to
CC	contain antibodies with one or more protein sequences or peptides cited
CC	above, forming an antibody-peptide complex comprising at least one of the
CC	protein sequences or peptides and the sample antibodies, and detecting
CC	the antibody-peptide complex. The protein sequences and method are useful
CC	for detecting and/or diagnosing HPV-associated epithelial cell
CC	abnormalities, precancerous conditions and cancers, such as cervical

CC cellular abnormalities selected from koilocytosis, hyperkeratosis,
 CC precancerous conditions encompassing intraepithelial lesions, high-grade
 CC dysplasias, invasive cancers and malignant cancers. The present sequence
 CC represents a specific example of a peptide derived from HPV 18 E6 early
 coding region.

XX Sequence 22 AA;

Query Match 100.0%; Score 120; DB 8; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCIDFGRIRERHYSDSYGD 22

Db 1 KCIDFGRIRERHYSDSYGD 22

RESULT 2

AAR14751 ID AAR14751 standard; protein; 32 AA.

XX AC AAR14751;

XX DT 28-JAN-1992 (first entry)

DE Seroreactive epitope #3 of HPV 18 protein E6.

XX PR vaccine; HPV18.

XX PA (BEHW) BEHRINGWERKE AG.

PI Bleul C, Gissmann L, Muller M;

XX DR WPI; 1991-334182/4/6.

XX PT New sero-reactive epitope(s) of human papilloma virus 18 proteins - and

PT corresp. proteins and antibodies, useful in vaccines and for diagnosis.

XX PS Claim 2; Page 5; 8pp; German.

XX This peptide can be used to identify antibodies specific to E6 protein.

CC It is also useful for a vaccine against HPV18. The E6 epitope was identified using anti-E6 serum to screen a recombinant phage expression library containing 100bp fragments of HPV18 DNA. The DNA insert is from

CC positive phage were sequenced and based on this information, overlapping decapeptides were prepared on polyethylene pins. They were tested (ELISA) against the antisera to locate the epitopes. See AAR14748-R14753

XX SQ Sequence 32 AA;

Query Match 92.5%; Score 111; DB 2; Length 32;

Best Local Similarity 95.5%; Pred. No. 7.7e-11;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGRIRERHYSDSYGD 22

Db 5 KCIDFGRIRERHYSDSYGD 26

RESULT 4
 AAR79656 ID AAR79656 standard; protein; 158 AA.

XX AC AAR79656;

XX DT 25-MAR-2003 (revised)

XX DT 06-DEC-1995 (first entry)

XX CS Homo sapiens.

XX PN WO9518974-A2.

XX PD 13-JUL-1995.

XX PF 04-JAN-1995;

XX PF 95WO-US000164.

AC AAR63866;

XX DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-JUN-1995 (first entry)

XX DE HPV18 E6/E7 proteins.

XX KW HPV; HPV18; E6 protein; E7 protein; diagnosis; cervical dysplasia;

CC cervix cancer.

XX OS Human Papillomavirus; strain 18.

XX XX Human Papillomavirus; strain 18.

XX PN WO9426334-A2.

XX PD 24-NOV-1994.

XX XX 06-MAY-1994; 94WO-US005085.

XX PR 06-MAY-1993; 93US-00058920.

XX PA (BAXT) BAXTER DIAGNOSTICS INC.

PI Brown JT;

XX DR WPI; 1995-006821/01.

XX DR P-PSDB; AAQ75471.

XX PR Human papilloma virus detection assay - by amplification using self sustained sequence replication and hybridisation with a detector probe.

PT PR disclosure; Page 27-28; 79pp; English.

XX PS Disclosure; Page 27-28; 79pp.

XX CC The sequences of the E6 and E7 polypeptide-encoding regions of human

CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded

CC proteins in AAR3365-66, respectively. Probes and primers based on these

CC sequences were used for HPV infection diagnosis; expression of E6 and E7

CC is diagnostic for cervical cancer or pre-malignant states. (Updated on

CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise

OS field.)

XX SQ Sequence 158 AA;

XX DR Query Match 92.5%; Score 111; DB 2; Length 158;

XX PR Best Local Similarity 95.5%; Pred. No. 4.6e-10;

XX PR Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX PR QY 1 KCIDFGRIRERHYSDSYGD 22

XX DR 67 KCIDFGRIRERHYSDSYGD 88

XX DR Query Match 92.5%; Score 111; DB 2; Length 158 AA.

XX PR Best Local Similarity 95.5%; Pred. No. 4.6e-10;

XX PR Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX PR QY 1 KCIDFGRIRERHYSDSYGD 22

XX DR 67 KCIDFGRIRERHYSDSYGD 88

XX DR Query Match 92.5%; Score 111; DB 2; Length 158 AA.

XX PR Best Local Similarity 95.5%; Pred. No. 4.6e-10;

XX PR Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX PR QY 1 KCIDFGRIRERHYSDSYGD 22

XX DR 67 KCIDFGRIRERHYSDSYGD 88

XX DR Query Match 92.5%; Score 111; DB 2; Length 158 AA.

XX PR Best Local Similarity 95.5%; Pred. No. 4.6e-10;

XX PR Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX PR QY 1 KCIDFGRIRERHYSDSYGD 22

XX DR 67 KCIDFGRIRERHYSDSYGD 88

XX DR Query Match 92.5%; Score 111; DB 2; Length 158 AA.

XX PR Best Local Similarity 95.5%; Pred. No. 4.6e-10;

XX PR Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX PR QY 1 KCIDFGRIRERHYSDSYGD 22

XX DR 67 KCIDFGRIRERHYSDSYGD 88

XX DR Query Match 92.5%; Score 111; DB 2; Length 158 AA.

XX PR Best Local Similarity 95.5%; Pred. No. 4.6e-10;

XX PR Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX PR QY 1 KCIDFGRIRERHYSDSYGD 22

XX DR 67 KCIDFGRIRERHYSDSYGD 88

XX	PR 04-JAN-1994;	94US-00176937.
XX	PR 23-MAY-1994;	94US-00247904.
XX	PR 27-MAY-1994;	94US-0050795.
XX	PR 13-SEP-1994;	94US-00305520.
PA	(MITO-) MITOTIX INC.	
XX	Draetta G, Rolfe M,	Eckstein JW, Cottarel G, Gyuris J;
XX	DR WPI; 1995-255137/33.	N-PSDB; AAQ97848.
XX	PT Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle	regulatory proteins - also new ubiquitin conjugating enzymes, their
PT	PT related nucleic acid, vectors, antibodies etc., useful for regulating	e.g. cell proliferation.
XX	PS Disclosure: Page 100-101; 157PP; English.	
XX	CC HPV-18 E6 cDNA (given in AAQ97848) was amplified from a HeLa cell cDNA	library using the primers given in AAQ97848-47. The gene was subcloned
CC	CC into a baculovirus vector for expression of recombinant E6 in SF9 insect	cells for use as a component of an in vitro ubiquitin conjugating system.
CC	(updated on 25-MAR-2003 to correct PN field.)	
XX	Sequence 158 AA;	
PS	Query Match 92.5%; Score 111; DB 2; Length 158;	
XX	Best Local Similarity 95.5%; Pred. No. 4.6e-10;	
DD	Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
PT	HPV-18 E6 Protein sequence..-	
XX	AAY39968 standard; protein; 158 AA.	
XX	AAY39968;	
AC	AC AC	
XX	AAV39968;	
DT	15-DEC-1999 (first entry)	
XX	HPV-18 E6 Protein sequence..-	
KW	Ubiquitin conjugating enzyme; Ubce; ubiquitin-mediated proteolysis;	
KW	cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis;	
KW	proliferative disorder; cancer; restenosis; tissue connective disorder;	
KW	wound healing; fibrosis disorder; rheumatoid arthritis; sclerodema;	
KW	insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;	
KW	diagnosis; therapy; E6.	
OS	Human papillomavirus.	
XX	US5968761-A.	
XX	19-OCT-1999.	
PD	07-JUN-1995;	95US-00486663.
XX	PR 04-JAN-1994;	94US-00176937.
XX	PR 23-MAY-1994;	94US-00247904.
PR	27-MAY-1994;	94US-00250795.
PR	13-SEP-1994;	94US-00305520.
XX	(MITO-) MITOTIX INC.	
PA	PA	
XX	Chiu MI, Cottarel G,	Berlin V, Damagnez V, Draetta G, Rolfe M;
PI	DR WPI; 1999-590402/50.	
XX	N-PSDB; AAZ27768.	

XX Identifying ubiquitination inhibitors using novel ubiquitin conjugating
PT enzymes.
XX Example 2; Col 89-92; 61PP; English.

XX This sequence is the human papillomavirus E6 protein. The invention
CC relates to assays for identifying an inhibitor of ubiquitin-mediated
CC proteolysis of a cell-cycle regulatory protein comprising contacting a
CC candidate agent with an ubiquitin-conjugating system and measuring a
CC level of ubiquitination. The ubiquitin-conjugating system comprises: (a)
CC a reconstituted protein mixture including a ubiquitin conjugating enzyme
CC (UbCE) produced by the expression of a nucleic acid which hybridizes
CC under high stringency conditions to human UbCE, *Candida albicans* UbCE,
CC *Schizosaccharomyces pombe* UbCE coding sequences; (b) a regulatory protein
CC ; and (c) ubiquitin. The polynucleotides are useful for identifying
CC ubiquitination inhibitors. The polynucleotides, polypeptides, antisense
CC compounds and antibodies against them may also be useful for the
CC treatment and/or diagnosis of proliferative disorders (e.g. cancer,
CC atherosclerosis, or restenosis), tissue connective disorders, controllin
CC wound healing, and disorders characterized by fibrosis (e.g. rheumatoid
CC arthritis, insulin dependent diabetes mellitus, glomerulonephritis,
CC cirrhosis, and scleroderma).

XX SQ Sequence 158 AA;

	Query Match	Score	Length
Qy	Best Local Similarity	92.5%	158
Db	Matches	95.5%	DB 2;
		Pred. No.	4.6e-10;
		Mismatches	0;
		Indels	0;
		Gaps	

	1	22
Qy	<chem>KCDEFGSIRELRYHSSDVSYGD</chem>	<chem>KCDEFGSIRELRYHSSDVSYGD</chem>
Db	67	88

XX RESULT 6
ID AAB03176 standard; protein; 158 AA.
XX AAB03176;
AC
XX DT 12-SEP-2003 (revised)
DT 23-OCT-2000 (first entry)
XX HPV-18 E6 protein.
DE
XX HPV-18 E6; ubiquitin mediated proteolysis; human;
KW cellular protein half life; ubiquitination inhibitor; p53; cyclin;
KW cell cycle regulator; myc deregulation; human papillomavirus;
KW HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia;
KW epidermal neoplasia; psoriasis; connective tissue disorder;
KW wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic.
XX OS Human papillomavirus; 18.
XX US6068932-A.
PN
XX 96US-00767942.
PD 30-MAY-2000.
PF 17-DEC-1996;
XX PR 04-JAN-1994; 94US-00176937.
PR 23-MAY-1994; 94US-00247904.
PR 27-MAY-1994; 94US-00250795.
PR 13-SEP-1994; 94US-00305520.
PR 07-JUN-1995; 95US-00486663.
XX PA (MITO-) MITOTIX INC.
XX Chiu MI, Cottarel G, Berlin V, Damagnez V, Rolfe M;
PI XX WPI; 2000-410854/35.

XX Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory
 PT protein for treating cancers involves measuring ubiquitination levels of
 PT the protein in the presence of candidate agent in an eukaryotic cell.
 XX Example 2; Col 97-100; 73pp; English.

CC The invention relates to a method of identifying an inhibitor of
 CC ubiquitin-mediated proteolysis of a cell cycle regulatory protein
 CC comprising contacting an engineered eukaryotic cell with a candidate
 CC agent. The eukaryotic cells is engineered to express a recombinant human,
 CC *Candida albicans* or *Schizosaccharomyces pombe* ubiquitin-conjugating
 CC enzyme (AAU3169-B03171), a cell cycle regulatory protein (such as p53)
 CC and ubiquitin. The specification also discloses novel *Candida albicans*
 CC and *Schizosaccharomyces pombe* ubiquitin-conjugating enzymes, caUBCE and
 CC spUBCE (AAU3170, AAU3171), and two novel human ubiquitin-conjugating
 CC enzymes, huBCE and rapUBC (AAU3169, AAU3173). The ubiquitin-mediated
 CC proteolysis system is the major pathway for the selective, controlled
 CC degradation of intracellular proteins in eukaryotic cells. In particular,
 CC this system controls the half-lives of cellular proteins, and is
 CC important in controlling the levels of proteins involved in cell cycle
 CC progression. Alterations in the ubiquitination of these proteins may
 CC therefore play a role in the development of cancers. For example, human
 CC papillomaviruses such as HPV-18 encode a transforming protein, E6
 CC (AAU03176), which combines with a cellular E6-associated protein (E6-AP;
 CC AAU03177) to stimulate the ubiquitination of p53, thus targeting it for
 CC degradation. The ubiquitination inhibitors identified according to the
 CC method of the invention are useful for treatment of cervical cancers and
 CC connective tissue disorders and for controlling the wound healing
 CC process. They are also useful in treatment of hyperplastic epidermal
 CC conditions such as psoriasis, neoplastic epidermal conditions, skin
 CC cancers e.g., basal cell carcinomas, squamous cell carcinomas. The
 CC inhibitors are useful for deregulating myc expression and rendering the
 CC cells sensitive to chemotherapeutic treatment or to upset the balance of
 CC transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-
 CC mediated degradation of cyclins are useful as antiproliferative agents.
 CC The present sequence represents HPV-18 E6 protein. (Updated on 12-SEP-
 CC 2003 to standardise OS field)

XX Sequence 158 AA;
 SQ Query Match 92.5%; Score 111; DB 3; Length 158;
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGRIRRLRHYSVYGD 22
 Db 67 KCIDFGRIRRLRHYSVYGD 88
 RESULT 8
 ID ADL90077 standard; protein; 158 AA.
 AC ADL90077;
 DT 17-JUN-2004 (first entry)
 DE Human papillomavirus 18-E6 protein, SEQ ID 17.
 KW Immune response; immunoglobulin; Ig; E6.
 OS Human papillomavirus.
 XX WO200417049-A2.
 XX 14-JUN-2001.
 PD 20-SEP-2002; 2002US-0412219P.
 XX 14-MAR-2003; 2003WO-US030188.
 PA (ASTRAL INC.
 XX 18-SEP-2003; 2003WO-US030188.
 PR 20-DEC-1999; 99US-0172705P.

PR 15-AUG-2000; 2000US-00641528.
 XX (EPIMINE INC.
 PA An isolated human papilloma virus (HPV) epitope, useful in vaccines for
 PT treating HPV infections.
 XX Disclosure; Page 22; 756PP; English.
 DR WPI; 2001-381497/40.
 XX PT
 PR
 XX PS
 CC The present invention describes an isolated prepared human papillomavirus
 CC (HPV) epitope (I), (I) has antiviral activity, and can be used in vaccine
 CC production. Peptides and corresponding nucleic acid compositions from the
 CC present invention are useful for stimulating an immune response to HPV by
 CC stimulating the production of CTL or HTL responses, specifically in the
 CC treatment or prophylaxis of HPV infections in persons who have not
 CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
 CC can also be used in a tetramer staining assay to assess peripheral blood
 CC mononuclear cells for the presence of antigen-specific CMs following
 CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
 CC recall responses or evaluate the efficacy of a vaccine. The vaccine
 CC compositions are useful for removing warts or treating HPV infections.
 CC The epitopes for inclusion in an epitope-base vaccine may be selected
 CC from conserved regions of viral or tumour-associated antigens, which
 CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
 CC that may be present in whole antigens can be avoided with the use of
 CC epitope-base vaccines. An additional advantage is the ability to combine
 CC selected epitopes (CMs and HTL) and to modify the composition of the
 CC epitopes achieving enhanced immunogenicity, the major benefit of the
 CC vaccine is that is safe and efficacious. AB98391 to AB98477 represent
 CC polypeptide sequences used in the exemplification of the present
 CC invention.
 XX Sequence 158 AA;

Query Match 92.5%; Score 111; DB 4; Length 158;
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KCIDFGRIRRLRHYSVYGD 22
 Db 67 KCIDFGRIRRLRHYSVYGD 88
 RESULT 8
 ID ADL90077 standard; protein; 158 AA.
 AC ADL90077;
 DT 17-JUN-2004 (first entry)
 DE Human papillomavirus 18-E6 protein, SEQ ID 17.
 KW Immune response; immunoglobulin; Ig; E6.
 OS Human papillomavirus.
 XX WO200417049-A2.
 XX 14-JUN-2001.
 PD 20-SEP-2002; 2002US-0412219P.
 XX 14-MAR-2003; 2003WO-US030188.
 PA (ASTRAL INC.
 XX 18-SEP-2003; 2003WO-US030188.
 PR 20-DEC-1999; 99US-0172705P.

XX WPI; 2004-295415/27.
 XX DR
 XX Generating an immune response to an antigen, useful for generating a desired T cell response comprising administering an immunoglobulin having one peptide epitope of the antigen attached to the immunoglobulin.
 PT XX Disclosure; Fig 1G; 154pp; English.
 PS XX
 SQ XX The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. The present sequence is an antigen sequence, used to illustrate the invention.
 XX Sequence 158 AA;

Query Match 92.5%; Score 111; DB 8; Length 158;
 Best Local Similarity 95.5%; Pred. No. 4.e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KCIDFGSRTRELRHYSYDSYGD 22
 Db 67 KCIDFYSRTRELRHYSYDSYGD 88

RESULT 9

ADO44074 ID ADO44074 standard; protein; 158 AA.
 XX AC ADO44074;
 XX DT 15-JUL-2004 (first entry)
 XX DE Amino acid sequence of the E6 polypeptide of HPV18.

XX KW E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer
 XX Human papillomavirus type 18.
 OS PN WO2004030636-A2.
 XX PD 15-APR-2004.
 XX PF 02-OCT-2003; 2003WO-US031726.
 XX PR 03-OCT-2002; 2002US-04159292.
 XX PA (AHRP) WYETH HOLDINGS CORP.
 XX PI Smith L, Cassetti MC;
 XX DR WPI; 2004-316328/29.
 XX PR New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.

XX Disclosure; Page 78; 101pp; English.

CC AD044074 AD044085 represent E6 polypeptides from human papillomaviruses. CC CC is the consensus sequence derived from these polypeptides. The specificitation describes human papillomavirus E6 and E7 polypeptides, CC where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are

CC useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.

XX SQ Sequence 158 AA;

Query Match 92.5%; Score 111; DB 8; Length 158;
 Best Local Similarity 95.5%; Pred. No. 4.e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KCIDFGSRTRELRHYSYDSYGD 22
 Db 67 KCIDFYSRTRELRHYSYDSYGD 88

RESULT 10

AAO22924 ID AAO22924 standard; protein; 172 AA.
 XX AC AAO22924;
 XX DT 12-DEC-2002 (first entry)
 XX DE Human papillomavirus-18 (HPV18) E66T-protein sequence.
 XX KW Viricide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine; fusion partner; immunogenicity; HPV infection; neoplasm; HPV18; human papillomavirus-18; E66T-sequence.
 XX CS Human papillomavirus.
 XX FN EP1243655-A1.
 XX PD 25-SEP-2002.
 XX PR 23-MAR-2001; 2001EP-00107271.
 XX PR 23-MAR-2001; 2001EP-00107271.
 XX PA (DEKR) DEUT KREBSFORSCHUNGSZENTRUM.
 XX PI Cid-Arregui A, Zur Hausen H;
 XX WPI; 2002-724552/79.
 XX DR N-PSDB; AAL53422.

XX Disclosure; Fig 4; 34pp; English.
 XX The invention relates to a new DNA sequence encoding a fusion protein comprising a mutagenized HPV (human Papillomavirus) E6 or E7 coding sequence and a sequence encoding a highly immunogenic fusion partner is useful to vaccinate against HPV infection.
 XX Disclosure; Fig 4; 34pp; English.
 XX The invention relates to a new DNA sequence encodes an E6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced by codons which lead to enhanced translation in a mammalian cell, containing a mutation which results in production of a truncated non-functional protein, and encoding a highly immunogenic polypeptide fusion partner capable of enhancing immunogenicity of the E6 or E7 protein in the mammalian host. The invention is used as a vaccine for the prevention or treatment of an HPV infection or a neoplasm associated with HPV infection. This sequence represents the human papillomavirus-18 (HPV18) E66T-protein sequence of the invention.

XX SQ Sequence 172 AA;
 Query Match 92.5%; Score 111; DB 5; Length 172;
 Best Local Similarity 95.5%; Pred. No. 5.e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 KCIDFGSRIRELRHYSVYGD 22	AY25385	ID AAY25385 standard; protein; 278 AA.
Db	73 KCIDFYSRIRERLRYSDVYGD 94	XX	XX
		AC AAY25385;	AC
		XX	XX
		DT 06-SEP-1999 (first entry)	DT
		XX	XX
		DE HPV fusion protein D1/3-E6-His/HPV18.	DE
		XX	XX
		KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response;	KW
		KW HPV antigen; prevention; treatment.	KW
		XX	XX
		OS Synthetic.	OS
		XX Human Papillomavirus.	XX
		PN WO933368-A2.	PN
		XX 08-JUL-1999.	XX
		PD 18-DEC-1998; 98WO-BP008563.	PD
		XX 24-DEC-1997; 97GB-00022262.	XX
		PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.	PA
		XX Dalemans WJJ, Gerard CMG;	XX
		PI WPI: 1999-405485/34.	PI
		XX DR N-PSDB; AAX78800.	XX
		PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to induce immune response to HPV.	PT
		XX Example XI: Page 59-60; 62pp; English.	XX
		XX AAY78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for preventing or treating HPV induced tumours	CC
		XX SQ Sequence 278 AA;	SQ
		PS Query Match Score 111; DB 2; Length 278;	PS
		XX Best Local Similarity 95.5%; Pred. No. 8.7e-10;	XX
		CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC
		Qy 1 KCIDFGSRIRELRHYSVYGD 22	Qy
		Db 178 KCIDFYSRIRELRHYSVYGD 199	Db
		RESULT 13 AAY02641 standard; protein; 278 AA.	RESULT 13
		XX DT 17-OCT-2003 (revised)	DT
		XX DF 22-JUN-1999 (first entry)	DF
		XX DE Prot.D1/3-E6-His/HPV18 protein.	DE
		XX KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;	KW
		XX OS Human Papillomavirus.	OS
		OS Haemophilus influenzae.	OS
		XX Chimeric.	XX
		RESULT 12	
Qy	1 KCIDFGSRIRELRHYSVYGD 22		
Db	68 KCIDFYSRIRERLRYSDVYGD 89		

PT	Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to induce immune response to HPV.	XX
XX	Example XI: Page 61-62; 62pp; English.	PS
XX	AAY78791-Y78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV represented in AAY23375-Y25386. These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for preventing or treating HPV induced tumours	CC
XX	Sequence 383 AA;	CC
SQ	Query Match 92.5%; Score 111; DB 2; Length 383; Best Local Similarity 95.5%; Pred. No. 1.2e-09; Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	CC
Qy	1 KCIDFGSRRELRYHSDSYVGD 22	CC
Db	178 KCIDFYSRRELRYHSDSYVGD 199	CC
RESULT 15		CC
AY02642	KCIDFGSRRELRYHSDSYVGD 22	CC
ID	AY02642 standard; protein; 383 AA.	CC
XX	Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for treatment or prophylaxis of HPV induced lesions.	CC
XX	Disclosure; Fig 22; 95pp; English.	CC
PS	This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutic treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)	CC
XX	Sequence 278 AA;	CC
SQ	Query Match 92.5%; Score 111; DB 2; Length 278; Best Local Similarity 95.5%; Pred. No. 8.7e-10; Matches 21; Conservative 1; Indels 0; Gaps 0;	CC
Qy	1 KCIDFGSRRELRYHSDSYVGD 22	CC
Db	178 KCIDFYSRRELRYHSDSYVGD 199	CC
RESULT 14		CC
AY25386	KCIDFGSRRELRYHSDSYVGD 22	CC
PN	W09910375-A2.	CC
XX	Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for treatment or prophylaxis of HPV induced lesions.	CC
XX	Disclosure; Fig 25; 95pp; English.	CC
XX	This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapy treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS Field)	CC
PS	Semience 383 AA.	CC
XX	SMITHKLINE BEECHAM BIOLOGICALS.	CC
XX	Bruck C., Cabezon Silva T., Delisse AEF, Gerard CMG; Lombardo-Benchikha A;	CC
XX	Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for treatment or prophylaxis of HPV induced lesions.	CC
XX	Disclosure; Fig 25; 95pp; English.	CC
XX	This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapy treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS Field)	CC
PS	Semience 383 AA.	CC
XX	SMITHKLINE BEECHAM BIOLOGICALS.	CC
XX	Dalemans WLJ, Gerard CMG;	CC
XX	WPI; 1999-405485/34.	CC
DR	N-FSDB; AAX78801.	CC

Query Match 92.5%; Score 111; DB 2; Length 383;
Best Local Similarity 95.5%; Pred. No. 1.2e-09;
Matches 21; Conservative 0; Mismatches -1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSDSVYCD 22
 ||||| ||||| ||||| |||||
Db 178 KCIDFYSRIRRLRHYSDSVYCD 199

Search completed: November 22, 2004, 20:27:28
Job time : 114.5 secs

GenCore version 5.1.6
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OM Protein - protein search, using SW model

Run on: November 22, 2004, 20:20:21 ; Search time 27.5 Seconds
 (without alignments)
 53.054 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDGSGRIRELRHYSVGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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 2: /cgnd_6_ptodata/1/iaa/5B_COMBO.PEP:/*
 3: /cgnd_6_ptodata/1/iaa/5A_COMBO.DEP:/*
 4: /cgnd_6_ptodata/1/iaa/6B_COMBO.DEP:/*
 5: /cgnd_6_ptodata/1/iaa/PCTUS_COMBO.PEP:/*
 6: /cgnd_6_ptodata/1/iaa/backfile1.PEP:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	111	92.5	32 1 US-08-466-285-4	Sequence 4, Appli
2	111	92.5	32 3 US-08-164-768-4	Sequence 4, Appli
3	111	92.5	158 2 US-08-247-904-10	Sequence 10, Appli
4	111	92.5	158 3 US-08-767-9424-19	Sequence 19, Appli
5	111	92.5	271 1 US-08-117-083-14	Sequence 14, Appli
6	111	92.5	278 3 US-09-485-885-21	Sequence 21, Appli
7	111	92.5	383 3 US-09-485-985-23	Sequence 23, Appli
8	68	56.7	162 1 US-08-316-239-4	Sequence 4, Appli
9	65	54.2	158 4 US-09-980-5231-2	Sequence 2, Appli
10	65	54.2	162 1 US-08-316-239B 3	Sequence 3, Appli
11	65	54.2	172 3 US-08-860-165-12	Sequence 12, Appli
12	65	54.2	172 3 US-08-860-165-14	Sequence 14, Appli
13	65	54.2	172 3 US-09-359-382-12	Sequence 12, Appli
14	65	54.2	172 3 US-09-359-382-14	Sequence 14, Appli
15	65	54.2	266 3 US-08-860-165-10	Sequence 10, Appli
16	65	54.2	266 3 US-09-359-382-10	Sequence 10, Appli
17	65	54.2	266 4 US-08-860-165-12	Sequence 1, Appli
18	65	54.2	273 3 US-09-485-885-4	Sequence 4, Appli
19	65	54.2	292 3 US-09-485-885-10	Sequence 10, Appli
20	65	54.2	371 3 US-09-485-985-6	Sequence 6, Appli
21	65	54.2	390 3 US-09-485-885-14	Sequence 14, Appli
22	47	39.2	10 3 US-08-159-329-88	Sequence 88, Appli
23	47	39.2	20 2 US-08-934-915-44	Sequence 44, Appli
24	47	39.2	20 2 US-08-934-915-163	Sequence 163, Appli
25	46.5	38.8	187 3 US-08-737-248-19	Sequence 19, Appli
26	46	38.3	347 4 US-08-928-796A-15125	Sequence 15125, Appli
27	46	38.3	1313 3 US-08-989-299-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
 US-08-466-285-4
 / Sequence 4, Application US/08466285
 / Patent No. 5753233
 / GENERAL INFORMATION:
 / APPLICANT: Bleul, Conrad
 / APPLICANT: Gissmann, Lutz
 / APPLICANT: Muller, Martin
 / TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of Human Papillomavirus (HPV)18
 / TITLE OF INVENTION: Human Papillomavirus (HPV)18
 / NUMBER OF SEQUENCES: 7
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Dunner
 / ADDRESS: Finnegan, Henderson, Farabow, Garrett & Dunn
 / STREET: 1300 I Street, N.W., Suite 700
 / CITY: Washington
 / STATE: D.C.
 / COUNTRY: USA
 / ZIP: 20005-3315
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC Compatible
 / OPERATING SYSTEM: PC-DC/MS-DOS
 / SOFTWARE: Patent Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/466,285
 / FILING DATE: 06-JUN-1995
 / CLASSIFICATION: 424
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/164,768
 / FILING DATE: 10-DEC-1993
 / CLASSIFICATION: 424
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/947,992
 / FILING DATE: 21-SEP-1992
 / CLASSIFICATION: 424
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/696,953
 / FILING DATE: 08-MAY-1991
 / CLASSIFICATION: 424
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: P 40 15 044.5
 / FILING DATE: 10-MAY-1990
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Manspeizer, David A.
 / REGISTRATION NUMBER: 37 540
 / REFERENCE/DOCKET NUMBER: 05552.1075-03000
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202)408-4000

TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-466-285-4

Query Match Score 111; DB 1; Length 32;
 Best Local Similarity 95.5%; Pred. No. 2.5e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRYSDSYGD 22
 Db 5 KCIDFYSRIRELRYSDSYGD 26

RESULT 2
 US-08-164-768-4 Application US/08164768
 ; Sequence 4, Application US/08164768
 ; Patent No. 6222794
 ; GENERAL INFORMATION:
 ; APPLICANT: BLEU, Conrad
 ; APPLICANT: GIESMANN, Lutz
 ; APPLICANT: MULLER, Martin
 ; TITLE OF INVENTION: SEROREACTIVE EPITOPOS ON PROTEINS OF
 ; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FINNIGAN, HENDERSON, FARABOW, GARRETT &
 ; STREET: DUNNER, L.L.P.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/164,768
 ; FILING DATE: 10-DEC-1993
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Forman, David S.
 ; REGISTRATION NUMBER: 33,694
 ; REFERENCE/DOCKET NUMBER: 05552.1075-020000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 32 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-164-768-4

Query Match Score 111; DB 3; Length 32;
 Best Local Similarity 95.5%; Pred. No. 2.5e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRYSDSYGD 22
 Db 5 KCIDFYSRIRELRYSDSYGD 26

US-08-247-904B-10
 Sequence 10, Application US/08247904B
 ; Parent No. 5981639
 ; GENERAL INFORMATION:
 ; APPLICANT: Rolfe, Mark
 ; APPLICANT: Eckstein, Jens W.
 ; APPLICANT: Draetta, Giulio
 ; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley, HOAG & Eliot
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02109
 ; COUNTRY: USA
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII (text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/247, 904B
 ; FILING DATE: 23-MAY-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: NIV-029.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 832-1000
 ; TELEFAX: (617) 832-7000
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 158 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-247-904B-10

Query Match Score 111; DB 2; Length 158;
 Best Local Similarity 95.5%; Pred. No. 1.4e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRYSDSYGD 22
 Db 67 KCIDFYSRIRELRYSDSYGD 88

RESULT 4
 US-08-767-912A-19
 Sequence 19, Application US/08767942A
 ; Patent No. 6058982
 ; GENERAL INFORMATION:
 ; APPLICANT: Rolfe, Mark
 ; APPLICANT: Chiu, M. Isabel
 ; APPLICANT: Terlin, Vivian
 ; APPLICANT: Damaguez, Veronique
 ; APPLICANT: Draetta, Giulio
 ; APPLICANT: Guillame, Corinne
 ; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/767,942A
 FILING DATE: 17-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MIV-029.04
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 158 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-767-942A-19

Query Match 92.5%; Score 111; DB 3; Length 158;
 Best Local Similarity 95.5%; Pred. No. 1.e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSIRRELHYSYGD 22
 Db 67 KCIDFYSIRRELHYSYGD 88

RESULT 5
 US-0-117-083-14
 Sequence 14, Application US/08117083
 Patent No. 5719054
 GENERAL INFORMATION:
 APPLICANT: Boursnell, Michael E.
 APPLICANT: Munro, Alan J.
 APPLICANT: Inglis, Stephen C.
 TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Walter H. Drexer
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/117,083
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Drexer, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-58783
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 271 amino acids
 TYPE: amino acid
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE: NAME/KEY: Protein
 LOCATION: 1..271

OTHER INFORMATION: /note= "Xaa refers to stop codon in
 OTHER INFORMATION: the open reading frame."
 US-08-117-083-14

Query Match 92.5%; Score 111; DB 1; Length 271;
 Best Local Similarity 95.5%; Pred. No. 2.4e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSIRRELHYSYGD 22
 Db 68 KCIDFYSIRRELHYSYGD 89

RESULT 6
 US-09-485-885-21
 Sequence 21, Application US/09485885
 Patent No. 6342224

GENERAL INFORMATION:
 APPLICANT: Bruck, Claudine
 APPLICANT: Cabazon Silva, Teresa
 APPLICANT: Delisse, Anne-Marie Eva Fernande
 APPLICANT: Gerard, Catherine Marie Ghislaine
 APPLICANT: Lombardo-Bencheikh, Angela
 TITLE OF INVENTION: Vaccine
 FILE REFERENCE: B45I07
 CURRENT APPLICATION NUMBER: US/09/485,885
 PRIOR APPLICATION NUMBER: PCT/EP98/05285
 PRIOR FILING DATE: 2000-02-18
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 21
 LENGTH: 278
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-485-885-21

Query Match 92.5%; Score 111; DB 3; Length 278;
 Best Local Similarity 95.5%; Pred. No. 2.5e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSIRRELHYSYGD 22
 Db 178 KCIDFYSIRRELHYSYGD 199

RESULT 7
 US-09-485-885-23
 Sequence 23, Application US/09485885
 Patent No. 6342224

GENERAL INFORMATION:
 APPLICANT: Bruck, Claudine
 APPLICANT: Cabazon Silva, Teresa
 APPLICANT: Delisse, Anne-Marie Eva Fernande
 APPLICANT: Gerard, Catherine Marie Ghislaine
 APPLICANT: Lombardo-Bencheikh, Angela
 TITLE OF INVENTION: Vaccine
 FILE REFERENCE: B45I07
 CURRENT APPLICATION NUMBER: US/09/485,885
 CURRENT FILING DATE: 2000-02-18
 PRIOR APPLICATION NUMBER: PCT/EP98/05285
 PRIOR FILING DATE: 1998-08-17
 PRIOR APPLICATION NUMBER: GB 9717953.5
 PRIOR FILING DATE: 1997-08-22
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 23
 LENGTH: 383
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-485-885-23

Query Match 8
Best Local Similarity 92.5%; Score 111; DB 3; Length 383;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGRIRRLRHYSVYGD 22
Db 178 KCIDFGRIRRLRHYSVYGD 199

RESULT 8
US -08-316-239B-4
Sequence 4, Application US/08316239B
Patent No. 5679509

GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
ATTORNEY: Parmenter, Cheryl A.
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an Increased Risk of Developing Cervical Dysplasia and Cervical Cancer

TITLE OF INVENTION: Methods and a Diagnostic Aid for Distinguishing a Subset of HPV that is Associated with an Increased Risk of Developing Cervical Dysplasia and Cervical Cancer

TITLE OF INVENTION: A Method and a Diagnostic Aid for Distinguishing a Subset of HPV that is Associated with an Increased Risk of Developing Cervical Dysplasia and Cervical Cancer

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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STREET: 6126 Rocky Way Court
CITY: Centreville
STATE: VA
COUNTRY: USA
ZIP: 20120-1400

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-4453
TELEFAX: (703) 803-9387

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: 162 amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO

US -08-316-239B-4

Query Match 9
Best Local Similarity 56.7%; Score 68; DB 1; Length 162;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGRIRRLRHYSVYGD 21
Db 72 KCLKFYSKISSEYRHYCYSVYGD 92

RESULT 9
US -09-980-523A-2
Sequence 2, Application US/09980523A
Patent No. 6783763

GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
ATTORNEY: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE

Query Match 54.2%; Score 65; DB 1; Length 162;
Best Local Similarity 57.1%; Pred. No. 0.018;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSVYG 21
Db 72 KCLKPFYSKISERHYCYSLYG 92

RESULT 11
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/110
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-12

Query Match 54.2%; Score 65; DB 3; Length 172;
Best Local Similarity 57.1%; Pred. No. 0.018;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSVYG 21
Db 10 KCLKPFYSKISERHYCYSLYG 30

RESULT 12
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/110
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-14

Query Match 54.2%; Score 65; DB 3; Length 172;

Matches	12;	Conservative	3;	Mismatches	6;	Indels	0;	Gaps	0;
Qy	1	KCIDFGSRIRERHYSRDSVYVG	21						
	:	:							
D _b	141	KCLKFYSKISSYRHYCISLYG	161						

RESULT 15
US-08-860-165-10
Sequence 10, Application US/08860165A
Patent No. 6004557

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/008668
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-10
Query Match 54.2%; Score 65; DB 3; Length 266;
Best Local Similarity 57.1%; Pred. No. 0.029;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Matches	1	KCIDFGSRIRERHYSRDSVYVG	21
	:	:	
D _b	72	KCLKFYSKISSYRHYCISLYG	92

Search completed: November 22, 2004, 20:33:43
Job time : 28.5 secs

endoglucanase I (E
 prolactin I - chum
 prolactin II - chu
 prolactin precurso
 prolactin precurso
 prolactin precurso
 prolactin precurso
 prolactin precurso
 prolactin - Atlan
 prolactin precurso
 prolactin, precurso
 lauric omega-hydr
 peptidyl-dipeptida
 probable hydrolase
 probable ingolase
 flagellin synthesi
 conserved hypothet
 conserv. omega-hydr

PSM protein - protein search, using SW model
Run on: November 22, 2004, 20:19:30 ; Search time 23.5 Seconds
 (without alignments)
 90.075 Million cell updates/s

Title:	US-10-612-818-5
Perfect score:	120
Sequence:	1 KCIDFGSRIRELRYHSDSYVD 22
Scoring table:	BLOSUM62
	Gapopen 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 KESUJI :
 W6WLB
 B6 Protein - human Papillomavirus type 18
 C.Species: human papillomavirus type 18

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A;Reference number: A91668; MUID:8721459; PMID:3034571
A;Accession: A21165

4: Pic4:
5: No. is the number of results predicted by chance to have a
6: score greater than or equal to the score of the result being printed,
7: and is derived by analysis of the total score distribution.

IMAPTES

Result No.	Score	Query Match	Length	ID	Description
1	111	92.5	158	1 W6WL18	E6 protein - human
2	96	80.0	158	2 S36561	E6 protein - human
3	75	62.5	158	1 W6WL39	E6 protein - human
4	71	59.2	158	1 W6WLPR	E6 protein - human
5	65	54.2	151	1 W6WL51	E6 protein - human
6	65	54.2	158	1 W6WLHS	E6 protein - human
7	64	53.3	149	1 W6WL33	E6 protein - human
8	63	52.5	153	2 S36503	E6 protein - human
9	62	51.7	154	2 S36527	E6 protein - human
10	60	50.0	149	1 W6WL35	E6 protein - human
11	60	50.0	149	1 W6WL58	E6 protein - human
12	59	49.2	148	2 A61237	E6 protein - human
13	59	49.2	148	2 S36515	E6 protein - human
14	59	49.2	148	2 S36573	E6 protein - human
15	58	48.3	150	2 S36544	E6 protein - human
16	57	47.5	149	1 W6WL31	E6 protein - human
17	56	46.7	155	1 W6WL56	E6 protein - human
18	56	46.7	155	2 A44890	E6 protein - human
19	56	46.7	191	1 W6WL81	E6 protein - human
20	55	45.8	153	1 S15621	E6 protein - human
21	54	45.0	150	2 W6WL42	E6 protein - human
22	54	45.0	159	1 S15614	E6 protein - human
23	54	45.0	159	2 S36497	E6 protein - human
24	51	42.5	211	2 S55129	E6 protein - human
25	50	41.7	142	2 S36509	E6 protein - human
26	50	41.7	410	2 T23264	E6 protein - human
27	49	40.8	936	2 T34024	E6 protein - human
28	48	40.0	155	1 W6WL43	E6 protein - human
29	47	39.2	190	2 S77248	E6 protein - human

A;Molecule type: DNA
A;Residues: 1-158 <COL>
A;Cross-references: GB:X05015; NID:960975; PIDN:CAA28664.1; PMID:560976
R;Matlasiakowski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pitt, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria
A;Reference number: A92791; PMID:318129
A;Contents: annotation of human papillomavirus type 18 E6 protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCC motif
F;105-141/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
Query Match 92.5%; Score 111; DB 1; Length 158;
Best Local Similarity 95.5%; Pred. No. 1e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy 1 KCIDDFSRIRLRYHSDSVYGD 22
Db 67 KCIDDFSRIRLRYHSDSVYGD 88
RESULT 2
S36561
E6 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36561
C;Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types
A;Reference number: S36469
A;Accession: S36561
A;Accession: S36561

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ALIGNMENTS

RESULT 1	
W6WL18	EEG protein - human papillomavirus type 18
C;Species:	human papillomavirus type 18
C;Accession:	30-Sep-1987 #sequence_revision 30
R;Seedorf, K.; Oltberman, T.; Kraemmer, C;	A26251; G26251
EBO J. 6, 139-144, 1987	
A;Title: Identification of early proteins	
A;Reference number: A91068; MUID:87218459	
A;Accession: A26165	
A;Molecule type: DNA	
A;Residues: 1-158 <SEE>	
A;Cross-references: UNIPROT:P06463; GB:X0	
R;Cole, S.T.; Danos, B.; Cole, R.J.	
J. Mol. Biol. 193, 599-608, 1987	
A;Title: Nucleotide sequence and comparat	
A;Reference number: A92937; MUID:87283882	
A;Accession: G26251	
A;Molecule type: DNA	
A;Residues: 1-158 <COL>	
A;Cross-references: GB:X05015; NID:960975	
R;Matlashewski, G.; Banks, L.; WuLiao, J	
J. Gen. Virol. 67, 1903-1916, 1986	
A;Title: The expression of human papillomavirus type 11 in African green monkey kidney cells	
A;Reference number: A22791; MUID:86306565	
A;Content: annotation; identification of	
C;Superfamily: papillomavirus E6 protein	
C;Keywords: DNA binding; early protein; t	
F122-68/Region: zinc finger CCC motif	
F1105-141/Region: zinc finger CCCC motif	
Qry	Query Match 92.5%; Score 1
Db	Best Local Similarity 95.5%; Pred. N Matches 21; Conservative 0; Missm
Qry	1 KCIDFGGSRELRLHYSRELRYDSVYGD 22
Db	67 KCIDFYSRTRRELRLHYSRELRYDSVYGD 88
RESULT 2	
S36561	EEG protein - human papillomavirus type 45
C;Species:	human papillomavirus type 45
C;Accession:	20-Feb-1985 #sequence_revision 20
R;Delius, H.; Hofmann, B.	S36561
E;Submitted to the EMBL Data Library, August	
A;Description: Primer-directed sequencing	
A;Reference number: S36469	
A;Accession: S36561	

A: Molecule type: DNA
 A: Residues: 1-158 <DBL>
 A: Cross-references: UNIPROT:P21735; EMBL:X74479; NID:9397022; PIDN:CAA52573.1; PMID:93970
 C: Superfamily: Papillomavirus E6 protein
 C: Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match Score 96%; DB 2; Length 158;
 Best Local Similarity 81.8%; Pred. No. 2.1e-07;
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSDSVYGD 22
 Db 67 KCIDFYSRIRELRYNSVSYGE 88

RESULT 3
 W6WL39
 E6 protein - human papillomavirus type 39
 C: Species: human papillomavirus type 39
 A: Note: host Homo sapiens (man)
 C: Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C: Accession: A38502
 R: Virology, C.; Strecker, R.E.
 R: Voelpel, C.; Strecker, R.E.
 A: Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
 A: Reference number: A38502; MUID:91135011; PMID:1847266

A: Status: translation not shown
 A: Molecule type: DNA
 A: Residues: 1-158 <VOL>
 A: Cross-references: UNIPROT:P24835; EMBL:M62849; NID:9333245; PIDN:AAA47050.1
 C: Superfamily: papillomavirus E6 protein
 C: Keywords: DNA binding; early protein; transforming protein; zinc finger

Query Match Score 75%; DB 1; Length 158;
 Best Local Similarity 73.7%; Pred. No. 0.00037;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CIDFGSSIRELRHYSDSVY 20
 Db 68 CIKFYAKIRELRYNSDGVY 86

RESULT 4
 W6WLPR
 E6 protein - human papillomavirus type ME180 (provirus)
 C: Species: human papillomavirus type ME180
 A: Note: host Homo sapiens (man)
 C: Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C: Accession: C41509
 R: Reuter, S.; Deibus, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
 J. Virol. 65, 5664-5668, 1991
 A: Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
 A: Reference number: A40509; MUID:91374616; PMID:1716694
 A: Status: translation not shown
 A: Molecule type: DNA
 A: Cross-references: UNIPROT:P27962; GB:M73258
 C: Superfamily: papillomavirus E6 protein
 C: Keywords: DNA binding; early protein; zinc finger

Query Match Score 71%; DB 1; Length 158;
 Best Local Similarity 68.4%; Pred. No. 0.0015;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CIDFGSRIRELRHYSDSVY 20
 Db 68 CIKFYAKIRELRYNSDGVY 86

RESULT 5
 W6WL51
 E6 protein - human papillomavirus type 51
 C: Species: human papillomavirus type 51
 A: Note: host Homo sapiens (man)
 C: Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C: Accession: E40415
 R: Junquu, O.; Crum, C.P.; Silverstein, S.J.
 J. Virol. 65, 4216-4225, 1991
 A: Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 51
 A: Reference number: A40415; MUID:91303675; PMID:1649326

A: Status: translation not shown
 A: Molecule type: DNA
 A: Residues: 1-151 <LUN>
 A: Cross-references: UNIPROT:P26554; GB:M62877
 C: Superfamily: Papillomavirus E6 protein
 C: Keywords: DNA binding; early protein; zinc finger
 P: 30-66/Region: zinc finger CCCC motif
 P: 103-139/Region: zinc finger CCCC motif

Query Match Score 65%; DB 1; Length 151;
 Best Local Similarity 61.9%; Pred. No. 0.012;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSDSVYGD 21
 Db 65 KCIDFYSRIRELRYNSVSYGE 85

RESULT 6
 W6WLHS
 Protein E6 - human papillomavirus type 16
 C: Species: human papillomavirus type 16
 A: Cross-references: UNIPROT:P0126; GB:K02718; NID:9333031; PIDN:AAA46939.1; PMID:9333032
 C: Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
 C: Accession: A03682; TI:0427
 R: Seedorff, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
 Virology 145, 181-185, 1985
 A: Title: Human papillomavirus type 16 DNA sequence.
 A: Reference number: A22355; MUID:8546220; PMID:2890099
 A: Molecule type: DNA
 A: Residues: 1-158 <SP1>
 A: Cross-references: UNIPROT:P0126; GB:K02718; NID:9333031; PIDN:AAA46939.1; PMID:9333032
 R: Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
 J. Virol. 65, 2093-2097, 1991
 A: Title: A negative element in the human papillomavirus type 16 genome acts at the level
 A: Reference number: 9116273; PMID:9116273
 A: Accession: TI:0427
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-158 <KEN>
 A: Cross-references: EMBL:K02718; NID:9333031; PIDN:AAA46939.1; PMID:9333032
 C: Genetics:
 C: Gene: E6
 C: Superfamily: papillomavirus E6 protein
 C: Keywords: DNA binding; early protein; zinc finger
 F: 77-73/Region: zinc finger CCCC motif
 F: 110-146/Region: zinc finger CCCC motif

Query Match Score 65%; DB 1; Length 158;
 Best Local Similarity 57.1%; Pred. No. 0.013;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSDSVYGD 21
 Db 72 KCIDFYSRIRELRYNSVSYGE 92

RESULT 7
 W6WL33

E6 protein - human papillomavirus type 33
 C;Species: human papillomavirus type 33
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A03683
 R;Ccde, S.T.; Streck, R.E.
 J. Virol. 58, 991-995, 1986
 A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh
 A;Reference number: A93020; MUID:86200464; PMID:3009902
 A;Molecule type: DNA
 A;Residues: 1-149 <COL>
 A;Cross-references: UNIPROT:P06427; GB:MI2732; NID:9333049; PIDN:AAA46958.1; PID:9463177
 C;Superfamily: Papillomavirus E6 Protein
 C;Keywords: DNA binding; early protein; zinc finger
 F:30-66/Region: zinc finger CCCC motif
 F:103-139/Region: zinc finger CCCC motif

Query Match 53.3%; Score 64; DB 1; Length 149;
 Best Local Similarity 57.1%; Pred. No. 0.017;
 Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CIDFGSRKRELHRYSDVYGD 22
 Db 66 CLRLFSKISEYRHNTSYVGN 86

RESULT 8
 S36503
 E6 protein - human papillomavirus type 30
 C;Species: human papillomavirus type 30
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 R;Dalius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36503
 A;Molecule type: DNA
 A;Residues: 1-153
 A;Cross-references: UNIPROT:P36809; EMBL:X74474; NID:9396973; PIDN:CAA52543.1; PID:93969
 C;Superfamily: Papillomavirus E6 Protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 52.5%; Score 63; DB 2; Length 153;
 Best Local Similarity 50.0%; Pred. No. 0.025;
 Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
 W6W158
 E6 protein - human papillomavirus type 58
 C;Species: human papillomavirus type 58
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36527

Query Match 50.0%; Score 60; DB 1; Length 149;
 Best Local Similarity 54.5%; Pred. No. 0.072%;
 Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KCIDFGSRKRELHRYSDVYGD 22
 Db 65 KCLLKFSKISEYRHNTSYVGE 86

RESULT 9
 S36527
 E6 protein - human papillomavirus type 53
 C;Species: human papillomavirus type 53
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 R;Dalius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36527
 A;Molecule type: DNA
 A;Residues: 1-154
 A;Cross-references: UNIPROT:P36815; EMBL:X74482; NID:9397046; PIDN:CAA52591.1; PID:93970
 C;Superfamily: Papillomavirus E6 Protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 51.7%; Score 62; DB 2; Length 154;
 Best Local Similarity 55.0%; Pred. No. 0.037%;
 Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CIDFGSRKRELHRYSDVYGD 22
 Db 66 CLRLFSKISEYRHNTSYVGN 86

RESULT 12

Qy 2 CIDFGSRIRELRHYSDSVYG 21
 Db 66 CLRFLSKISERHYQYSLYG 85

Best Local Similarity 49.2%; Score 59; DB 2; Length 148;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Query Match 2 CIDFGSRIRELRHYSDSVYG 21
 Best Local Similarity 55.0%; Pred. No. 0.1;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CIDFGSRIRELRHYSDSVYG 21
 Db 66 CLRFLSKISERHYQYSLYG 85

Best Local Similarity 49.2%; Score 59; DB 2; Length 148;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

RESULT 13

S36515 E6 protein - human papillomavirus type 34
 C;Species: human papillomavirus type 34
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 A;Cross-references: UNIPROT:P36811; EMBL:X74476; NID:9396989; PID:CAA52555.1; PID:g3969
 C;Superfamily: Papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Molecule type: DNA
 A;Residues: 1-148 <TAK>
 C;Superfamily: papillomavirus E6 protein

Query Match 2 CIDFGSRIRELRHYSDSVYG 21
 Best Local Similarity 50.0%; Pred. No. 0.1;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CIDFGSRIRELRHYSDSVYG 21
 Db 67 CLIFYSKVRQFRRYNQSYG 86

Best Local Similarity 49.2%; Score 59; DB 2; Length 148;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

RESULT 14

S36573 E6 protein - human papillomavirus type 52
 C;Species: human papillomavirus type 52
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S36573
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36573
 A;Molecule type: DNA
 A;Residues: 1-148
 A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:9397038; PID:CAA52585.1; PID:g3970
 C;Superfamily: Papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger
 Query Match 49.2%; Score 59; DB 2; Length 148;
 Best Local Similarity 55.0%; Pred. No. 0.1;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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GenCore version 5.1.6

OM Protein - protein search, using sw model

Run on: November 22, 2004, 20:32:01 ; Search time 97.5 Seconds
(without alignments)
79.906 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFSSRIRLRYHSDSYVGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing First 45 summaries

Database : Published Applications AA:
 1: /cn2_6_ptodata/1/pubpa/us07_pubcomb.pep:
 2: /cn2_6_ptodata/1/pubpa/pct_new_pub_pep:
 3: /cn2_6_ptodata/1/pubpa/us06_pub_pep:
 4: /cn2_6_ptodata/1/pubpa/us05_pub_pep:
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 6: /cn2_6_ptodata/1/pubpa/pctus_pubcomb.pep:
 7: /cn2_6_ptodata/1/pubpa/us08_new_pub_pep:
 8: /cn2_6_ptodata/1/pubpa/us09a_pubcomb.pep:
 9: /cn2_6_ptodata/1/pubpa/us09b_pubcomb.pep:
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 11: /cn2_6_ptodata/1/pubpa/us09c_pubcomb.pep:
 12: /cn2_6_ptodata/1/pubpa/us09c_new_pub_pep:
 13: /cn2_6_ptodata/1/pubpa/us10a_pubcomb.pep:
 14: /cn2_6_ptodata/1/pubpa/us10b_pubcomb.pep:
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 17: /cn2_6_ptodata/1/pubpa/us10e_pubcomb.pep:
 18: /cn2_6_ptodata/1/pubpa/us11_new_pub_pep:
 19: /cn2_6_ptodata/1/pubpa/us60_new_pub_pep:
 20: /cn2_6_ptodata/1/pubpa/us60_pubcomb.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	22	16	US-10-612-818-5	Sequence 5, Appli
2	92.5	172	16	US-10-437-963-102875	Sequence 6, Appli
3	92.5	278	13	US-10-320-797-3356	Sequence 21, Appli
4	92.5	383	13	US-10-000-903-23	Sequence 23, Appli
5	56.7	151	14	US-10-177-390-6	Sequence 6, Appli
6	54.2	171	16	US-10-472-724-2	Sequence 2, Appli
7	54.2	266	9	US-03-367-309A-1	Sequence 1, Appli
8	54.2	273	13	US-10-000-903-4	Sequence 4, Appli
9	54.2	292	13	US-10-000-903-10	Sequence 10, Appli
10	54.2	371	13	US-10-000-903-6	Sequence 6, Appli
11	54.2	390	13	US-10-000-903-14	Sequence 14, Appli
12	50	417	20	US-10-476-570-12	Sequence 12, Appli
13	40.8	936	14	US-10-363-493-5053	Sequence 5053, Appli

ALIGNMENTS

RESULT 1
US-10-612-818-5
; Sequence 5, Application US/10612818
; PUBLICATION NO. US2004011025A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papillomavirus Infection
; TITLE OF INVENTION: Associated Cancers
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10-612-818
; PRIORITY FILING DATE: 2003-07-01
; PRIORITY APPLICATION NUMBER: US 60/394,172
; PRIORITY FILING DATE: 2002-07-02
; PRIORITY FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: / OTHER INFORMATION: Derived from the E6 early coding region of HPV 18
; US-10-612-818-5

Query Match 100.0%; Score 120; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCIDFSSRIRLRYHSDSYVGD 22
Dy 1 KCIDFSSRIRLRYHSDSYVGD 22
Dy 1 KCIDFSSRIRLRYHSDSYVGD 22

RESULT 2

US-10-472-724-6
 Sequence 6, Application US/10472724
 Publication No. US20040171B6A1
 GENERAL INFORMATION:
 APPLICANT: Cid-Arregui, Angel
 APPLICANT: Zur Hausen, Harald
 TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 FILE REFERENCE: B45107
 CURRENT APPLICATION NUMBER: US/10/000,903
 CURRENT FILING DATE: 2001-10-01
 PRIOR APPLICATION NUMBER: PCT/EP98/05285
 PRIOR FILING DATE: 1998-08-17
 PRIOR APPLICATION NUMBER: GB 9717953.5
 PRIOR FILING DATE: 1997-08-22
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 6
 LENGTH: 172
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-000-903-23

FEATURE:
 OTHER INFORMATION: Synthetic Construct

US-10-472-724-6

Query Match 92.5%; Score 111; DB 16; Length 172;
 Best Local Similarity 95.5%; Pred. No. 3.7e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSDSYGG 22
 Db 73 KCIDFYSRIRELRHYSDSYGG 94

RESULT 5

US-10-177-390-6
 Sequence 6, Application US/10177390
 Publication No. US20030143743A1
 GENERAL INFORMATION:
 APPLICANT: Schuler, Gerold
 APPLICANT: N.V. Antwerp Innovatiecentrum
 TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
 FILE REFERENCE: 021505wo/JH/ml
 CURRENT APPLICATION NUMBER: US/10/177,390
 CURRENT FILING DATE: 2002-06-20
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 151
 TYPE: PRT
 ORGANISM: Human papillomavirus type 16
 US-10-177-390-6

Query Match 56.7%; Score 68; DB 14; Length 151;
 Best Local Similarity 61.9%; Pred. No. 0.016;
 Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSDSYGG 21
 Db 65 KCIDFYSRIRELRHYCSYVG 85

RESULT 6

US-10-472-724-2
 Sequence 2, Application US/10472724
 Publication No. US20040171B6A1
 GENERAL INFORMATION:
 APPLICANT: Cid-Arregui, Angel
 APPLICANT: Zur Hausen, Harald
 TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 FILE REFERENCE: 4121-154

Query Match 92.5%; Score 111; DB 13; Length 278;
 Best Local Similarity 95.5%; Pred. No. 6.3e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRHYSDSYGG 22
 Db 178 KCIDFYSRIRELRHYSDSYGG 199

RESULT 4

US-10-000-903-23
 Sequence 23, Application US/10000903
 Publication No. US20020182221A1

```

; SEQ ID NO 4 ; LENGTH: 273
; TYPE: PRT ; ORGANISM: Homo sapien
US-10-000-903-4

Query Match 54.2%; Score 65; DB 13; Length 273;
Best Local Similarity 57.1%; Pred. No. 0.09;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRYHSDSYVG 21
Db 178 KCLKPFYSKISEYRHYCYSLYG 198

RESULT 9
US-10-000-903-10
Sequence 10, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine ; Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match 54.2%; Score 65; DB 13; Length 292;
Best Local Similarity 57.1%; Pred. No. 0.09;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRYHSDSYVG 21
Db 197 KCLKPFYSKISEYRHYCYSLYG 217

RESULT 10
US-10-000-103-6
Sequence 6, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine ; Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT

RESULT 8
US-10-000-903-4
Sequence 4, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine ; Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT

; SEQ ID NO 27
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 54.2%; Score 65; DB 16; Length 171;
Best Local Similarity 57.1%; Pred. No. 0.054;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRYHSDSYVG 21
Db 77 KCLKPFYSKISEYRHYCYSLYG 97

RESULT 7
US-09-367-309B-1
Sequence 1, Application US/09367309A
Publication No. US2002008329A1
GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIARD, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 54.2%; Score 65; DB 9; Length 266;
Best Local Similarity 57.1%; Pred. No. 0.087;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRELRYHSDSYVG 21
Db 72 KCLKPFYSKISEYRHYCYSLYG 92

RESULT 8
US-10-000-903-4
Sequence 4, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine ; Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT

```

; ORGANISM: Homo sapien
 US-10-000-903-6
 Query Match 54.2%; Score 65; DB 13; Length 371;
 Best Local Similarity 57.1%; Pred. No. 0.13; Gaps 0;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 KCIDFGRIRERHYSDSYVG 21
 Db 178 KCLKFYSKISETRHYCYSLYG 198

RESULT 11
 US-10-000-903-14
 ; Sequence 14, Application US/10000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Fernande
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 14
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-000-903-14

Query Match 54.2%; Score 65; DB 13; Length 390;
 Best Local Similarity 57.1%; Pred. No. 0.13; Gaps 0;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 KCIDFGRIRERHYSDSYVG 21
 Db 197 KCLKFYSKISETRHYCYSLYG 217

RESULT 12
 US-10-476-570-12
 ; Sequence 12, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLERE, Bernard
 ; APPLICANT: BOURGAULT-VILLARD, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: papillomavirus Proteins and uses thereof
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 12
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: artificial sequence

; FEATURE: OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
 US-10-476-570-12
 Query Match 41.7%; Score 50; DB 16; Length 20;
 Best Local Similarity 58.8%; Pred. No. 1.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 5 FGSRIREHRYSDSYVG 21
 Db 1 FYSKISSETRHYCYSLYG 17

RESULT 13
 US-10-369-493-5053
 ; Sequence 5053, Application US/10369493
 ; Publication No. US2003033675A1
 ; GENERAL INFORMATION
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10152052B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 5053
 ; LENGTH: 936
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-5053

Query Match 40.8%; Score 49; DB 14; Length 936;
 Best Local Similarity 36.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Qy 2 CIDFGSIRELRYDSYVG 20
 Db 324 CTOFGGSYLDASHFSDTFF 342

RESULT 14
 US-09-220-091-3
 ; Sequence 3, Application US/09220091
 ; Patent No. US200200452A1
 ; GENERAL INFORMATION
 ; APPLICANT: H. Robert Horvitz
 ; APPLICANT: Craig Cao
 ; APPLICANT: Xiaowei Lu
 ; TITLE OF INVENTION: A TUMOR SUPPRESSOR PATHWAY IN C. ELEGANS
 ; FILE REFERENCE: 01997/200203
 ; CURRENT APPLICATION NUMBER: US/09/220,091
 ; CURRENT FILING DATE: 1998-12-23
 ; EARLIER APPLICATION NUMBER: 60/047,996
 ; EARLIER FILING DATE: 1997-05-28
 ; EARLIER APPLICATION NUMBER: 09/087,136
 ; EARLIER FILING DATE: 1998-05-28
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 3
 ; LENGTH: 961
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-09-220-091-3

Query Match 40.8%; Score 49; DB 9; Length 961;
 Best Local Similarity 36.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CIDFSSRIRLRYHSDSVY 20
 Db 349 CTOEGGSVLDARRHSDHTF 367

RESULT 15
 US-10-437-963-102875
 ; Sequence 102875, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(5321)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 102875
 ; LENGTH: 605
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_100359C.1.pep
 US-10-437-963-102875

Query Match 40.0%; Score 48; DB 16; Length 605;
 Best Local Similarity 33.3%; Pred. No. 95;
 Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 CIDFSSRIRLRYHSDSVYGD 22
 Db 372 CVERGQRLLWYKHSDETLDD 392

Search completed: November 22, 2004, 20:48:54
 Job time : 97.5 secs

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OM protein - protein search, using sw model						
Run on: November 22, 2004, 20:18:17 ; Search time 127.5 Seconds (without alignments) 99.280 Million cell updates/sec						
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5						
Searched: 1825181 seqs, 57537446 residues						
Total number of hits satisfying chosen parameters: 1825181						
Minimum DB seq length: 0 Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries						
Database : UniProt_02: 1: uniprot_sprot: 2: uniprot_trembl: *						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	92.5	VE6 HPV18	1	158	Q9DNPB	human papillomavirus type 18 E6 protein in bacteria
2	92.5	VE6 HPV18	2	158	AAP20594	"Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";
3	92.5	VE6 HPV18	2	158	P21735	"Nucleotide sequence of human papillomavirus type 18 E6 protein in bacteria and the production of anti-E6 antibodies.";
4	96.0	VE6 HPV18	1	158	O9Y4Y4	human sapien
5	96.0	VE6 HPV18	2	158	O10608	human papillomavirus type 18 E6 protein in HeLa cells";
6	96.0	VE6 HPV18	2	158	Q81964	SEQUENCE FROM N.A. ;
7	71.1	VE6 HPV18	2	158	Q9WbG0	SEQUENCE FROM N.A. ;
8	68.3	VE6 HPV18	2	158	P50804	SEQUENCE FROM N.A. ;
9	67.5	VE6 HPV18	2	158	P24835	SEQUENCE FROM N.A. ;
10	75.0	VE6 HPV18	2	158	Q91R59	SEQUENCE FROM N.A. ;
11	73.0	VE6 HPV18	2	151	O994a0	SEQUENCE FROM N.A. ;
12	73.0	VE6 HPV18	2	151	Q994a0	SEQUENCE FROM N.A. ;
13	71.1	VE6 HPV18	1	158	Q919C0	SEQUENCE FROM N.A. ;
14	71.0	VE6 HPV18	2	158	Q919C2	SEQUENCE FROM N.A. ;
15	71.0	VE6 HPV18	2	158	Q919C8	SEQUENCE FROM N.A. ;
16	71.0	VE6 HPV18	2	158	Q919D2	SEQUENCE FROM N.A. ;
17	71.0	VE6 HPV18	2	162	Q919d3	SEQUENCE FROM N.A. ;
18	68.0	VE6 HPV18	2	151	Q919e2	SEQUENCE FROM N.A. ;
19	68.0	VE6 HPV18	2	151	Q919e4	SEQUENCE FROM N.A. ;
20	68.0	VE6 HPV18	2	130	Q919f3	SEQUENCE FROM N.A. ;
21	68.0	VE6 HPV18	2	130	Q919f5	SEQUENCE FROM N.A. ;
22	68.0	VE6 HPV18	2	130	Q919f6	SEQUENCE FROM N.A. ;
23	68.0	VE6 HPV18	2	138	Q919f7	SEQUENCE FROM N.A. ;
24	68.0	VE6 HPV18	2	143	Q919f8	SEQUENCE FROM N.A. ;
25	68.0	VE6 HPV18	2	151	Q919f9	SEQUENCE FROM N.A. ;
26	68.0	VE6 HPV18	2	151	Q919f10	SEQUENCE FROM N.A. ;
27	68.0	VE6 HPV18	2	151	Q919f11	SEQUENCE FROM N.A. ;
28	68.0	VE6 HPV18	2	151	Q919f12	SEQUENCE FROM N.A. ;
29	68.0	VE6 HPV18	2	151	Q919f13	SEQUENCE FROM N.A. ;
30	68.0	VE6 HPV18	2	151	Q919f14	SEQUENCE FROM N.A. ;
31	68.0	VE6 HPV18	2	151	Q919f15	SEQUENCE FROM N.A. ;

RT	"B6 protein of human papillomavirus type 18 binds zinc.";	DR	InterPro; IPR001334; B6.
RL	Oncogene 4:1089-1093 (1989).	DR	Pfam; PF00518; B6; 1.
RN	[7]	SEQUENCE	158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;
RP	INTERACTION WITH FBNL1, AND INHIBITION OF B6-MEDIATED TRANSFORMATION.	Query Match	92.5%; Score 111; DB 2; Length 158;
RX	MEIDLINE=22188366; PubMed=1220142; DOI=10.1016/S0006-291X(02)0041-7;	Best Local Similarity	95.5%; Pred. No. 7e-09;
RA	Du M., Fan X., Hong E., Chen J.J.;	Matches	21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RA	RT	Qy	1 KCIDFGSRRIRLRYHSVYGD 22
RL	Interaction of oncogenic Papillomavirus E6 proteins with fibulin-1.";	Db	67 KCIDFYSRIRLRYHSVYGD 88
- -	Biochem. Biophys. Res. Commun. 296:1962-1969 (2002).		
CC	- - FUNCTION: This protein has transforming activity in vitro.		
CC	- - PROTEIN: Exhibits a strong, but non specific affinity for double		
CC	- - stranded DNA (in vitro).		
CC	- - SUBCELLULAR LOCATION: Interacts with FBNL1.		
CC	- - NUCLEAR MATRIX-ASSOCIATED.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	RESULT 3	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	ID	AA20594 PRELIMINARY; PRT; 158 AA.
CC	the European Bioinformatics Institute. There are no restrictions on its	AC	AA20594; 01-MAR-2004 (TREMBLrel. 27, Created)
CC	use by non-profit institutions as long as its content is in no way	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
CC	modified and this statement is not removed. Usage by and for commercial	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)
CC	entities requires a license agreement (see http://www.isb-sib.ch/announces/) or send an email to license@isb-sib.ch).	DB	E6 protein.
CC	OS Human Papillomavirus type 18.	OS	Human Papillomavirus type 18.
CC	OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;	OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
DR	EMBL; X04334; CAA27819.1; -.	NCBI_TaxID=10582;	
DR	EMBL; X05015; CRA99511.1; -.	OX	
DR	EMBL; M20323; AAA99511.1; -.	RN [1]	SEQUENCE FROM N.A.
DR	M26798; AAA46946.1; -.	RA	Burk R.D., Chen Z., Burk R.D., "The newly modified full genome sequence of HPV18 prototype (Cole, 1987), with E6, E7, E1, E2, E4, E5, L2 and L1 ORFs."
DR	EMBL; X041773; CRA98466.1; -.	RT	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; A063324; CRA00531.1; -.	RL	EMBL; AY262282; AAP20594.1; -.
DR	EMBL; A063285; CRA00542.1; -.	DR	SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;
DR	PIR; A26165; W6PNL18.	SQ	SEQUENCE FROM N.A.
DR	InterPro; IPR001334; B6.	Query Match	92.5%; Score 111; DB 2; Length 158;
DR	Pfam; PF00518; B6; 1.	Best Local Similarity	95.5%; Pred. No. 7e-09;
KW	XN Early protein; Nuclear protein; Oncogene; Zinc-finger.	Matches	21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
FT	ZN_FING	Qy	1 KCIDFGSRRIRLRYHSVYGD 22
FT	ZN_FING	Db	67 KCIDFYSRIRLRYHSVYGD 88
FT	32		
FT	CONFFLICT		
FT	22		
FT	105		
FT	68		
FT	Potential.		
SQ	SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;	RESULT 4	
Query Match	92.5%; Score 111; DB 1; Length 158;	VE6 HPV45 STANDARD; PRT; 158 AA.	
Best Local Similarity	95.5%; Pred. No. 7e-09;	AC	221735; STANDARD; PRT; 158 AA.
Matches	21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DT	01-MAY-1991 (Rel. 18, Created)
DE	1 KCIDFGSRRIRLRYHSVYGD 22	DT	01-JUN-1994 (Rel. 29, Last sequence update)
OS	67 KCIDFYSRIRLRYHSVYGD 88	DE	05-JUL-2004 (Rel. 44, Last annotation update)
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;	DN	Name=EV.
OC	Papillomavirus.	OS	Human Papillomavirus type 45.
OC	NCBI_TaxID=10582;	OC	Viruses; dsDNA viruses, no RNA stage; Papillomavirus.
RN	SEQUENCE FROM N.A.	OC	Papillomavirus.
RA	Kisseljev F.; Laassri M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,	RN [2]	SEQUENCE FROM N.A.
RA	Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and	RP	
RT	Transformation Potential of E7 Gene and its Mutants.";	RA	Kaplan J.B., Burk R.D., Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
RT	Virus Genes 182:139-149(1999).	RA	Hofmann B.; Delius H., "Prime-directed sequencing of human papillomavirus types. "
RL	RN SEQUENCE FROM N.A.	RR	Curr. Top. Microbiol. Immunol. 186:13-31(1994).
RN	RA Kisseljev F.; Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and	CC	- - FUNCTION: This protein has transforming activity in vitro.
RA	Transformation Potential of E7 Gene and its Mutants.";	CC	- - PROTEIN: This protein has transforming activity in vitro.
RA	Virus Genes 182:139-149(1999).	CC	- - SUBSTRATE: Stranded DNA (in vitro).
RA	RN SEQUENCE FROM N.A.	CC	- - SUBCELLULAR LOCATION: Nuclear matrix-associated.
RA	RA Kisseljev F.; Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RL	Transformation Potential of E7 Gene and its Mutants.";	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
DR	GO; GO:0002025; C:host cell nucleus; IEA.	DR	
DR	GO; GO:0003677; F:DNA binding; IEA.	DR	

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01-JUL-1997 (TREBLErel. 04, Last sequence update)
 01-OCT-2003 (TREBLErel. 25, Last annotation update)
 Oncoprotein B6
 Human papillomavirus type 45.
 Viruses: dsDNA viruses, no RNA stage; Papillomaviridae;
 Viruses: dsDNA viruses, no RNA stage; Papillomaviridae;

RESULT 5					
2974Y4	09Y4Y4	PRELIMINARY;	PRT;	158 AA.	
AC	OPYAYA4,				
DDT	OPYAYA4,				
DT	01-NOV-1999	(TREMBLref. 12, Created)			
DT	01-NOV-1999	(TREMBLref. 12, Last sequence update)			
DT	01-OCT-2003	(TREMBLref. 25, Last annotation update)			
DE	E6 protein.				
DN	Name=HPV45_E6;				
DS	Homo sapiens (Human).				
DS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
DOC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TAXID	9606;				
[1]					
RP	SEQUENCE FROM N.A.				
RA	Sastre-Garcia X., Favre M., Couturier J., Orth G.,				
RT	"Distinct patterns of alteration of myc genes associated with integration of human papillomavirus type 16 or type 45 in two genital tumours.";				
RT	J. Gen. Virol. 81:198-199 (2000).				
RL					

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[2]RN
    SEQUENCE FROM N.A.
    RRP
    FAYRE M.G.; Submitted (JUN-1999) to the EMBL/GenBank/DBBJ databases.
    RRI
    GO:00042055; C:host cell nucleus; IEA.
    GO:0003677; F:DNA binding; IEA.
    InterPro:IPR001344; B6.
    Pfam:PF0051; E6_1.
    DR
    SEQUENCE 158 AA; 18914 MW; A61AEF98390AEBB3 CRC64;
    ISQ

Query Match          80.0% ; Score 96; DB 2; Length 158;
Best Local Similarity 81.8%; Pred. No. 1.4e-06;
Matches 18; Conservative 3; Mismatches 1; Indels 0;
Gaps 0;

Qy      1 KCIDFGSRIRELYHSDSYGD 22
Dy      67 KCTDFEYSSRREYVYSNSVY 88

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RESULT 6
 Q10608 Q10608 PRELIMINARY;
 IID O10608; PRT;
 O10608;
 AAC 01-1111-1997 [REDACTED] 04 Created

DT 01-JUL-1997 (TREMBLrel_04; Last sequence update)
 DT 01-OCT-2003 (TREMBLrel_25; Last annotation update)
 DE Oncoprotein_E6.
 RA Human papillomavirus type 45.
 OS Viruses; dsDNA viruses; no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBITaxID=10593;
 RN [1] SEQUENCE FROM N.A.
 RA Saxe-Garau X., Favre M., Couturier J., Orth G.;
 RT "Distinct patterns of alteration of myc genes associated with
 RT integration of HPV16 or HPV45 DNA in two genital tumors.";
 RL J. Gen. Virol. 0:0-0(0).
 RN [2] SEQUENCE FROM N.A.
 RA Favre M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; Y13218; CAA73660.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Interpro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 DR Sequence 158 AA; 18914 MW; A61AEF98390AEEB3 CRC64;
 Query Match 80.0%; Score 96; DB 2; Length 158;
 Best Local Similarity 81.8%; Pred. No. 1.4e-06;
 Matches 18; Conservative 3; Mismatches 1; Indels 0;
 Qy 1 KCIDFGSRIRELRHYSVYGD 22
 Db 67 KCIDFGSRIRELRHYSVYGE 88
 RESULT 7
 Q81964 PRELIMINARY; PRT; 160 AA.
 ID Q81964
 AC Q81964;
 DT 01-NOV-1996 (TREMBLrel_01; Created)
 DT 01-NOV-1996 (TREMBLrel_01; Last sequence update)
 DT 01-OCT-2003 (TREMBLrel_25; Last annotation update)
 DE ORF putative E6 protein.
 GN Name=ORF putative E6;
 RA Human papillomavirus type 59.
 RA Viruses; dsDNA viruses; no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBITaxID=37115;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE-94103229; PubMed=8030222;
 RX RA Rho J., Roy-Burnam A., Kim H., de Villiers E.M., Matsukura T.
 RA Choie J.;
 RT "Nucleotide sequence and phylogenetic classification of human
 RT papillomavirus type 59.";
 RL Virology 203:158-161 (1994).
 DR EMBL; X77858; CA54849.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Interpro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 DR Sequence 160 AA; 19042 MW; B060020AFD530A16 CRC64;
 Query Match 71.7%; Score 86; DB 2; Length 160;
 Best Local Similarity 68.2%; Pred. No. 5e-05;
 Matches 15; Conservative 4; Mismatches 3; Indels 0;
 Qy 1 KCIDFGSRIRELRHYSVYGD 22
 Db 67 KCISFYARVEKRYRDSVYGE 88

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CC
 DR EMBL; M73258; -; NOT_ANNOTATED_CDS.
 DR PIR; C40500; NWLPR.
 DR InterPro; IPR001334; E6.
 DR PFam; PF0518; E6; 1.
 DR DNA-binding; Early protein; Nuclear protein; Zinc-finger.
 FT 32 68 Potential.
 FT 106 141 Potential.
 SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;

Query Match 59.2%; Score 71; DB 1; Length 158;
 Best Local Similarity 68.4%; Pred. No. 0.01;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CIDFGSRIREPHYSDSVY 20
 Db 68 CIKFYAKIREPYYSSSVY 86

RESULT 15

Q7KYK8 PRELIMINARY; PRT; 158 AA.
 AC Q7KYK8;
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human Papillomavirus type 68.
 OC dsDNA viruses; no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID:452440;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:91374616; PubMed:1716694;
 RA Reuter S., Delius H., Kahn T., Hofmann B., zur Hausen H., Schwarz E.;
 RT "Characterization of a novel human papillomavirus DNA in the cervical carcinoma cell line ME180".
 RL J. Virol. 65:5564-5568(1991).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98090464; PubMed:9427755;
 RA Reuter S., Bartelmann M., Vogt M., Geissen C., Napieralski T., Kahn T.,
 RA Delius H., Lichten P., Weltz S., Korn B., Schwarz E.;
 RT "APM-1, a novel human gene, identified by aberrant transcription with papillomavirus oncogenes in a cervical carcinoma cell line, encodes a BTB/POZ-zinc finger protein with growth inhibitory activity".
 RL EMBO J. 17:215-222(1998).
 DR EMBL; Y14591; CAA7431.1; -.
 DR InterPro; IPR001334; E6.
 DR PF0518; E6; 1.

SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;
 Query Match 59.2%; Score 71; DB 2; Length 158;
 Best Local Similarity 68.4%; Pred. No. 0.01;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CIDFGSRIREPHYSDSVY 20
 Db 68 CIKFYAKIREPYYSSSVY 86

age block (uspi)